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(54) Title: VIRULENCE GENES, PROTEINS, AND THEIR USE

(57) Abstract: Virulence genes of *Yersinia* species are identified that encode products which may be of use in therapy or diagnosis. The genes are identified as SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 57, 58 and 64.

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VIRULENCE GENES, PROTEINS, AND THEIR USE

Field of the Invention

This invention relates to virulence genes and proteins, and their use. More particularly, it relates to genes and proteins/peptides obtained from *Yersinia pseudotuberculosis*, and their use in therapy and in screening for drugs.

Background of the Invention

Yersinia pseudotuberculosis is an organism that is implicated in gastroenteritis, terminal ileitis and mesenteric adenitis in humans and Yersiniosis in livestock. It is desirable to provide a means for treating or preventing conditions caused by *Yersinia pseudotuberculosis*, e.g. by immunisation.

Summary of the Invention

The present invention is based on the discovery of virulence genes in *Yersinia* species, in particular, *Yersinia pestis* and *Yersinia pseudotuberculosis*.

According to a first aspect of the invention, a peptide of the invention is encoded by a gene comprising any of the nucleotide sequences identified herein as SEQ ID NOS. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 57, 58 and 64, or a homologue thereof in a Gram-negative bacterium having at least 60% sequence similarity or identity at the peptide or nucleotide level, or a functional fragment thereof, for therapeutic or diagnostic use.

The peptide has many therapeutic uses for treating *Yersinia* infections, including use in vaccines for prophylactic application.

According to a second aspect of the invention, a polynucleotide encoding a peptide defined above, is also useful for therapy or diagnosis.

According to a third aspect of the invention, a gene that encodes the peptide is utilised to prepare an attenuated microorganism. The attenuated microorganism has a mutation that disrupts the expression of a gene identified herein, to provide a strain that lacks virulence. This microorganism will also have use in therapy and diagnosis.

According to a fourth aspect of the invention, a peptide, gene or attenuated microorganism of the invention is used in the preparation of a medicament for the treatment or prevention of a condition associated with infection by *Yersinia* or Gram-negative bacteria, e.g. gastroenteritis.

According to a fifth aspect of the invention, a vaccine comprises a peptide of the invention, in a suitable diluent, excipient or pharmacologically acceptable buffer. The vaccine is used in therapy to treat or prevent infection by *Yersinia* or Gram-negative bacteria.

According to a sixth aspect of the invention, an antibody is raised against a peptide of the invention. The antibody can be used in immunotherapy to treat infection.

According to a seventh aspect of the invention, a peptide, polynucleotide or microorganism of the invention is used in an assay to screen for potential antimicrobial drugs.

Description of the Invention

The present invention is based on the discovery of genes encoding peptides which are implicated in virulence. A peptide and gene of the invention is therefore useful for the preparation of therapeutic agents to treat infection. It should be understood that references to therapy also include preventative treatments, e.g. vaccination. Furthermore, while the products of the invention are intended primarily for treatment of infections in human patients, veterinary applications are also considered to be within the scope of the invention.

The present invention is described with reference to *Yersinia pseudotuberculosis*. However, all the *Yersinia* strains, and many other Gram-negative bacterial strains, are likely to include related peptides or proteins having amino acid sequence identity or similarity to those identified herein. Organisms likely to contain the peptide include, but are not limited to the genera *Salmonella*, *Enterobacter*, *Klebsiella*, *Shigella* and *Yersinia*.

In a preferred embodiment, the peptides comprise the *Yersinia pseudotuberculosis* amino acid sequence that corresponds to that disclosed herein for *Yersinia pestis*.

Preferably, the peptides that may be useful in the various aspects of the invention have greater than a 60% similarity with the peptides identified herein. More preferably, the peptides have greater than 80% sequence similarity. Most preferably, the peptides have greater than 90% sequence similarity, e.g. 95% similarity. With regard to the polynucleotide sequences identified herein, related polynucleotides that may be useful in the various aspects of the invention have greater than 60% identity with the sequences identified herein. More preferably, the polynucleotide sequences have greater than 80% sequence identity. Most preferably, the polynucleotide sequences have greater than 90% sequence identity, e.g. 95% identity.

The terms "similarity" and "identity" are known in the art. The use of the term "identity" refers to a sequence comparison based on identical matches between correspondingly identical positions in the sequences being compared. The term "similarity" refers to a comparison between amino acid sequences, and takes into account not only identical amino acids in corresponding positions, but also functionally similar amino acids in corresponding positions. Thus similarity between polypeptide sequences indicates functional similarity, in addition to sequence similarity.

Levels of identity between gene sequences and levels of identity or similarity between amino acid sequences can be calculated using known methods. In relation to the present invention, publicly available computer based methods for determining identity and similarity include the BLASTP, BLASTN and FASTA (Atschul *et al.*, J. Molec. Biol., 1990; 215:403-410), the BLASTX program available from NCBI, and the Gap program from Genetics Computer Group, Madison WI. The levels of similarity and identity provided herein, were obtained using the Gap program, with a Gap penalty of 12 and a Gap length penalty of 4 for determining the amino acid sequence comparisons, and a Gap penalty of 50 and a Gap length penalty of 3 for the polynucleotide sequence comparisons.

Having characterised a gene according to the invention, it is possible to use the gene sequence to search for related genes or peptides in other microorganisms. This may be carried out by searching in existing databases, e.g. EMBL or GenBank.

Peptides or proteins according to the invention may be purified and isolated by methods known in the art. In particular, having identified a gene sequence, it will be possible to use recombinant techniques to express the gene in a suitable host. Active fragments and related molecules can be identified and may be useful in therapy. For example, a peptide or its active fragment may be used as an antigenic determinant in a vaccine, to elicit an immune response. They may also be used in the preparation of antibodies, for passive immunisation, or diagnostic applications. Suitable antibodies include monoclonal antibodies, or fragments thereof, including single-chain Fv fragments. Methods for the preparation of antibodies will be apparent to those skilled in the art.

Active fragments are those that retain a biological function of the peptide or which generate antibodies that are specific for that peptide. For example, when used to elicit an immune response, the fragment will be of sufficient size, such that antibodies generated from the fragment will discriminate between that peptide and other peptides of the bacterial microorganism. Typically, the fragment will be at least 30 nucleotides (10 amino acids) in size, preferably 60 nucleotides (20 amino acids) and most preferably greater than 90 nucleotides (30 amino acids) in size.

It should also be understood, that in addition to related molecules from other microorganisms, the invention encompasses modifications made to the peptide and polynucleotide identified herein which do not significantly alter its biological role. It will be apparent to the skilled person that the degeneracy of the genetic code can result in polynucleotides with minor base changes from those specified herein, but which nevertheless encode the same peptide. Complementary polynucleotides are also within the invention. Conservative replacements at the amino acid level are also envisaged, i.e. different acidic or basic amino acids may be substituted without substantial loss of function.

Included within the scope of the claimed invention are molecules that comprise a polynucleotide which hybridizes under stringent hybridization conditions to a portion of a polynucleotide of the invention. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150 nM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

By a "polynucleotide which hybridizes to a portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridization to at least 15 nucleotide bases, and more preferably at least 20 nucleotide bases, still more preferably at least 30 nucleotide bases, and even more preferably 30-70 (e.g. 50) nucleotide bases of the reference polynucleotide.

The preparation of vaccines based on attenuated microorganisms is known to those skilled in the art. Vaccine compositions can be formulated with suitable carriers or adjuvants, e.g. alum, as necessary or desired, to provide effective immunisation against infection. The preparation of vaccine formulations will be apparent to the skilled person. The attenuated microorganisms may be prepared with a mutation that disrupts the expression of a gene identified herein. The skilled person will be aware of methods for disrupting expression of particular genes. Techniques that may be used include insertional inactivation or gene deletion techniques. Attenuated microorganisms according to the invention may also comprise additional mutations in other genes, for example in a gene required for growth of the microorganism, e.g. an *aro* mutation.

Attenuated microorganisms may also be used as carrier systems for the delivery of heterologous antigens, therapeutic proteins or nucleic acids (DNA or RNA). In this embodiment, the attenuated microorganisms are used to deliver a heterologous antigen, protein or nucleic acid to a particular site *in vivo*. Introduction of a heterologous antigen, peptide or nucleic acid into an attenuated microorganism can be carried out by conventional techniques, including the use of recombinant constructs, e.g. vectors, which comprise polynucleotides that express the heterologous antigen or therapeutic protein, and also include a suitable promoter sequence. Alternatively, the gene that encodes the heterologous antigen or protein may be incorporated into the genome of the organism and an endogenous promoter used to control expression.

More generally, and as is well known to those skilled in the art, a suitable amount of an active component of the invention can be selected, for therapeutic use, as can suitable carriers or excipients, and routes of administration. These factors will be chosen or determined according to known criteria such as the nature/severity of the condition to be treated, the type and/or health of the subject etc.

In a separate embodiment, the products of the invention may be used in screening assays for the identification of potential antimicrobial drugs or for the detection for virulence. Routine screening assays are known to those skilled in the art, and can be adapted using the products of the invention in the appropriate way. For example, the products of the invention may be used as the target for a potential drug, with the ability of the drug to inactivate or bind to the target indicating its potential antimicrobial activity.

The various products of the invention may also be used in veterinary applications.

The following is a summary of the experimental procedure used to identify the virulence genes. The full experimental procedure and results have now been published in Karlyshev *et al.*, Infection and Immunity, 2001; 69(12): 7810-7819.

The virulence genes of the invention were identified using a modified version of the signature-tagged mutagenesis (STM) method (Hensel *et al.*, Science, 1995; 269: 400-403), to screen a *Yersinia pseudotuberculosis* mutant bank for attenuated mutants, in a murine model of Yersiniosis infection. Bacteria containing a transposon insertion within a virulence gene failed to be recovered from mice inoculated with a mixed population of mutants.

The transposons used in the method contained DNA tages that were amplified using biotinylated primers and hybridised to high-density oligonucleotide arrays containing DNA complementary to the tags. Comparison of the hybridisation signals from input pools and output pools identified mutants whose relative abundance was significantly reduced in the output pool.

The sequence data from the transposon insertion regions was then compared to the complete *Yersinia pestis* C092 genome sequence.

Bacterial strains and growth conditions:

Y. pseudotuberculosis YPIII pIB1 strain (Rosquist *et al.*, Nature, 1988; 334: 522-525) was maintained in Luria Broth (LB) and LB agar containing nalidixic acid (40 µg ml^{-1}). *E. coli* XL2 Blue MRF' (Stratagene), used in cloning experiments, were grown overnight at 37°C on LB agar plates. For selection, agar plates were supplemented with the antibiotics kanamycin (50 µg ml^{-1}), ampicillin (100 µg ml^{-1}), tetracycline (10 µg ml^{-1}) or nalidixic acid. *E. coli* CC118(λ*pir*) (Herrero *et al.*, J. Bacteriol, 1990; 172: 6557-6567) was used as a host strain for maintenance of the *pir*-dependent pUT mini-Tn5Km2 vector (de Lorenzo *et al.*, J. Bacteriol., 1990; 172: 6568-6572) in cloning experiments. The helper strain *E. coli* S17/pNJ5000 was maintained as described in Grinter *et al.*, Gene, 1983; 21: 133-143.

Construction of double-tagged mini-Tn5 transposon mutants:

Tag-sequences were chosen from those that had been shown to work well in similar experiments with *Saccharomyces cerevisiae* (Winzeler *et al.*, Science, 1999; 285: 901-906). The sequences of the 192 PCR primers (primer A and primer B) and the preparation of plasmids carrying tagged mini-Tn5 transposons are shown in Karlyshev *et al.*, 2001, *supra*.

Conjugation:

Initial triple mating experiments of *E. coli* CC118 (λ*pir*) donor strain, transformed with the plasmids carrying tagged mini-Tn5, and *Y. pseudotuberculosis* using a helper strain *E. coli* S17/pNJ5000 (Grinter *et al.*, 1984, *supra*) were performed as described in Oyston *et al.*, Microbiology, 1996; 142: 1847-1853. Direct mating experiments (without a helper strain) using *E. coli* 19851 *pir*$^{+}$ as the donor strain were performed as described in Metcalf *et al.*, Plasmid, 1996; 35: 1-13. Exconjugants were selected for kanamycin and nalidixic acid resistance. Both the recipient strain, YPIII pIB1, and the exconjugants were checked for the presence of the virulence plasmid using Congo red magnesium oxalate (CRMOX) plates (Riley *et al.*, J. Clin. Microbiol., 1989; 27: 213-214. All attenuated transposon derivatives grew as predominantly small red colonies, confirming that they retained the virulence plasmid.

Tag sequence detection:

Genomic DNA was extracted and the tags identified according to the protocol in Karlyshev *et al.*, 2001, *supra*.

In vivo experiments:

Three input pools containing 60, 40 and 33 transposon mutants respectively, were constructed and stored at -70°C. Aliquots (0.1 ml) containing approximately 10^7 cfu were inoculated into 10 ml LB and incubated with shaking overnight at 30°C. The overnight culture (2 ml) was used to inoculate 20 ml of fresh pre-warmed LB and further incubated at 37°C for 3 hours with shaking.

Genomic DNA was isolated from approximately 10^8 cells and stored (input pool). Bacteria were pelleted at 3,000 x g and diluted in Phosphate buffered saline (PBS) for infection and viable count determination. Pairs of eight-week-old female Balb/c mice were challenged intravenously (iv) via the tail vein with 10^5 or $5x10^5$ cfu. After 3 days, the surviving mice were culled, spleens were removed and homogenized in 3 ml of LB using a stomacher (Seward Medical Ltd) on maximum setting for 5 minutes. Dilutions of the extracts were plated on LB agar containing kanamycin and nalidixic acid. Plates containing approximately 10^4 colonies were washed with saline, mixed and aliquots were taken for making lysates (for PCR) or for total DNA preparation. Genomic DNA recovered from the spleens were the output pools.

Mutants with reduced survival *in vivo* were visualised by comparing the scanned images from arrays that had been hybridized with tags amplified from the input pools with images obtained from two independent output pools.

The input and output pools of the mutants were compared by hybridizing the labeled amplified tags to high-density oligonucleotide arrays (Affymetrix) containing complementary DNA sequences. The hybridization patterns were found to be reproducible. Mutants that showed reduced signals in the output pool for both tags in duplicate mice were selected for further analysis.

Characterization of attenuated mutants and identification of the transposon insertion sequences:

Approximately 5% out of 603 exconjugants exhibited a statistically valid reduction of signal intensity. Transposon insertion sites in the selected mutants were sequenced using a single primer PCR sequencing procedure (Karlyshev *et al.*, BioTechniques, 2000; 28: 1078-1082). The results are summarized in Tables 1 and 2. The *Y. pestis* genome sequence database (http://www.sanger.ac.uk/Projects/Y_*pestis*/) was used for identification of the corresponding genes in that pathogen; almost 100% identity of the *Y. pseudotuberculosis* sequences to the *Y. pestis* DNA sequences implies similarity in their function. The YPO number is the accession number that is used to identify the gene in the *Y. pestis* genome sequence database. The SEQ ID NOS. 1-58 and 64 are the *Yersinia pestis* sequences. SEQ ID NOS. 35, 56, 57 and 58 are genes in *Y. pestis* that appear to be non-functional in that they appear to contain many mutations in the gene sequence that disrupt the expression of an amino acid product. However, the orthologue (homologue) in *Y. pseudotuberculosis*.

is expected to be functional. The reference to "nrdb" refers the non-redundant amino acid database (www.blast.genome.ad.jp). Any orthologue found in this database is indicated in the columns to the right of the nrdb value.

Certain gene sequences had no orthologue in *Y. pestis*. These genes are identified herein by the mutant number 5D12, 5H10, 5B12, 1A9-1 and 1C9. The sequence provided herein for these mutants is not the complete gene sequence but is the flanking sequence of the transposon insertion site in *Yersinia pseudotuberculosis*. This sequence may not be part of the virulence gene but may be an upstream regulatory site. The flanking sequence is used to identify a suitable site for mutation that will result in a loss of virulence in the microorganism. Accordingly, mutant microorganisms can be prepared which have an attenuating mutation within the sequence identified herein.

In addition to the preparation of attenuated microorganisms, the encoded products of the genes identified herein are suitable as targets for immunotherapy or as immunogenic components of vaccines. In this context, the products identified by the references 5E4, 2G8, 5G6, 1D12, 5G7, 1A9, 4H2, 3G1, 5A5, 3F10, 2B3, 1H6, 2G5, 3G6, 2G10, 1H9, 4F4 and 4G11, are all preferred as they are located on the outer or inner membrane, or are extracellular proteins, shown in Table 3. In Table 3, IM, PP, OM and EC denote inner membrane, periplasmic, outer membrane and extracellular, respectively.

Table 1.

Mutant	SEQ ID NO.	*In vivo* CI	*In vitro* CI	Similarity, *Y. pestis* (%)	*Y. pestis* ORF	Similarity, nrdb (%)	Product	Microorganism
4H9	1	0.03	0.06	97	YPO0054	85	glycosyltransferase	*S. marcescens*
2B3	3	1.02	0.85	94	YPO0337	NS	-	-
5E4	5	NT	NT	99	YPO0702	46	putative lipoprotein	*Mycobacterium tuberculosis*
30	7	0.48	0.31	98	YPO1108	91	citrate synthase	*S. typhimurium*
2G8	9	0.53	1.34	96	YPO1174	39	Adhesin	*E. coli*
3C10	11	0.055	1.02	98	YPO1186	66	hypothetical	*E. coli*
3H10	13	0.08	0.07	97	YPO1382 (promoter region)	43	LpsA, glycosyltransferase	*Pasteurella haemolytica*
5G6	15	0.021	0.88	95	YPO1987	NS	-	-
1D12	17	0.084	1.34	97	YPO1994	NS	-	-
1H10	19	NT	NT	98	YPO2174	62	UDP-glucose 6-dehydrogenase	*Rhizobium meliloti*
4H10	21	0.0036	1.95	96	YPO2287a	65	ABC-transporter	*Methanococcus jannaschii*
5G7	23	0.25	1.09	98	YPO2440	82	iron(III) dicitrate ATP-binding protein	*Haemophilus influenzae*
1A9	25	NT	NT	100	YPO2532	NS	-	-
4H2	27	NT	NT	98	YPO2712	77	RseA, negative regulator of RpoE (sigma 24)	*E. coli*
5E6	56	0.27	1.24	97	YPO3004	47	Pro-dipeptidase	*B. subtilis*
1D2	29	0.43	0.08	96	YPO3099	100	ManC, mannose-1-P guanylyltransferase	*Y. pseudotuberculosis*
3G2	57	0.13	NT	98	YPO3100	100	Fcl, fucose synthetase	*Y. pseudotuberculosis*
1B3	31	0.29	0.98	90	YPO3104	100	O-antigen polymerase	*Y. pseudotuberculosis*
1D9	58	NT	0.07	98	YPO3114	100	DdhB, CDP-D-glucose-dehydratase	*Y. pseudotuberculosis*
3F3	33	0.04	0.44	95	YPO3116	100	AscD, ascarilose biosynthesis	*Y. pseudotuberculosis*
3G1	35	0.21	1.25	97	YPO3144	89	MdlB, Multi-drug resistance protein	*E. coli*
5A5	36	0.44	1.16	98	YPO3572	88	hypothetical transcription factor	*E. coli*

1G6	38	NT	NT	97	YPO3657 (intergenic)	NS	Unknown	-
3F10	40	0.017	0.46	99	YPO3834	87	PldA, phospholipase A	*E. coli*
1G6-1	42	NT	0.41	96	YPO3965	47	VirA, His kinase	*Agrobacterium tumefaciens*
5D12	59	0.003	0.98	NS	-	80	Wzx	*S. typhimurium*
5H10	60	NT	NT	NS	-	70	phage-related transcription activator	*Xylella fastidiosa*
5B12	61	0.89	1.32	NS	-	59	hypothetical	*phage HP1*
1A9-1	62	NT	NT	NS	-	NS	Unknown	-
1C9	63	NT	0.36	NS	-	NS	Unknown	-
1G6a	64	NT	NT	100	YPO03657a	-	YhdT	*E. coli*

Table 2

Mutant	SEQ ID NO.	Orthologue in *Y. Pestis*
2G5	44	YPO1485
3G6	46	YPO2503
2G10	48	YPO1483
1H9	50	YPO1696
4F4	54	YPO0036
4G11	52	YPO3010

Table 3

Mutant	Orthologue in *Y. pestis*	Orthologue in nrdb	Gene name	YP product size, aa	subcellular location[1]
1H6	YPO3965	VirA, *Agrobacterium tumefaciens*, 9e-30	*virA*	851	IM
3F10	YPO3834	PldA, *S. typhimurium*, e-127	*pldA*	292	OM
2G8	YPO1174	low score similarities to C-term domains of various OM proteins	-	309	OM
5G7	YPO2440	YfeB, *H. influenzae*, e-111	*yfeB*	296	IM
3G1	YPO3144	MdlB, *E. coli*, e0.0	*MdlB*	607	IM
2B3	YPO0337	no simil.	-	141	OM
5G6	YPO1987	putative PP of *S. typhimurium*, e-146	-	552	?
1D12	YPO1994	no simil.	-	316	?
5A5	YPO3572	Putative EC protein of *S. enterica*, 2e-91	-	207	PP or OM
4H2	YPO2712	RseA	*rseA*	218	
1A9	YPO2532	no simil.	-	-	?
5E4	YPO0702	low similarity to various putative secreted proteins of the same size		331	OM or PP
2G5	YPO1485	hyp. protein VCA0110 *V. cholerae*, 3e-66	-	587	?
3G6	YPO2503	no simil.	-	222	?
2G10	YPO1483	no simil.	-	533	?
1H9	YPO1696	various usher proteins	-	815	OM
4F4	YopH	YopH	*yopH*	468	EC
4G11	YPO3010	YopM Y. ent.	*yopM-2*	410	EC

Genes involved in polysaccharide biosynthesis:

One third of the sequenced mutants had transposon insertions in genes related to polysaccharide biosynthesis (mainly LPS core or O-antigen biosynthesis). In five cases (1B3, 1D2, 1D9, 3G2 and 3F3; Table 1) the genes disrupted belong to a single characterized O-antigen biosynthesis locus of *Y. pseudotuberculosis*. The disrupted genes encode mannose-phosphate-guanylyl transferase YPO3099 (1D2), fucose synthetase YPO3100 (3G2), LPS core biosynthesis protein YPO3104 (1B3), sugar dehydratase YPO3114 (1D9) and ascarylose biosynthesis protein YPO3116 (3F3). These genes are also present in *Y. pestis*. Other genes related to polysaccharide biosynthesis, such as those encoding UDP-glucose 6-dehydrogenase (1H10) and glycosyltransferase (4H9) were also identified. One mutant, 3H10, contained an insert in a putative promoter region of a single-gene operon encoding glycosyltransferase. The only mutation in an LPS-related gene which was absent in *Y. pestis* encoded an O-antigen transporter (5D12).

Putative virulence-related genes with orthologues in other bacteria:

Putative interrupted virulence genes include those encoding phospholipase A (*pldA*) (3F10), sensory transducer His kinase VirA (1G6-1), a putative adhesin (2G8), a Pro-dipeptidase (5E6), RseA, a negative regulator of sigma 24 transcription factor (4H2) a transcription activator (5H10) and a transcription regulator (5A5) flanked by a *vspC* gene essential for secretion of virulence factors. The genes found in 4H10 and 3G1 are related to ABC transporters, a large class of proteins involved in export-import of a range of molecules. A clue to their possible function can be found from the analysis of corresponding regions of *Y. pestis*. In the case of 3G1, other genes of the operon are involved in ammonia assimilation. These genes are assumed to be essential *in vivo*, when bacteria have a depleted source of nitrogen. Similarly, the *Y. pestis* orthologue of the gene disrupted in the ABC transporter (4H10) is also located in the region involved in nitrate, as well as amino acid, transport. An unusual feature of this region in *Y. pestis* is that this gene overlaps by 270 nucleotides with another gene (AMP nucleosidase) transcribed in the opposite direction. Disrupted genes in the iron-III dicitrate ATP-binding protein 5G7 is likely to be involved in iron transport.

Unknown and hypothetical genes:

Six mutants (1G6, 5D12, 5H10, 5B12, 1A9-1 and 1C9) contained inserts into genes with unknown function. Two of them (1C9 and 1A9-1) did not have counterparts in *Y. pestis*. Both these mutants contained inserts in the region identical to an *E. coli* integrase-recombinase pseudogene, but actually had inserts into an adjacent region similar to an *E. coli* gene with unknown function. Transposon integration sites in these mutants, were separated by approximately 200 nucleotides. A region flanking the insertion site in the 1G6 appeared to be unique for *Yersinia* as it had 97% identity in the *Y. pestis* database, whereas no similarity to other bacteria was found. Genes in mutants 3C10 and 5B12 have similarities in a non-redundant database (nrdb) and also have counterparts in *Y. pestis*. The genes inactivated in mutants 2B3, 5G6, 1D12 and 1A9 appear to be unique for *Yersinia*, as no homologues could be identified in a nrdb. Genes inactivated in certain mutants do not have *Y. pestis* orthologues. One of these mutants (5D12) contains insert in the gene encoding a putative O-antigen transferase (see above).

In vivo and *in vitro* competition studies:

For *in vivo* competition studies, mutant and wild-type strains were grown separately to exponential phase in LB media with appropriate antibiotics. Bacteria were washed with LB media and the concentration adjusted to $5x10^6$ cfu/ml. Equal volumes of each bacterial suspension were mixed together and 0.1 ml volumes were injected iv into 4 mice as above. Viable counts on LB, LB-Nal and LB-Nal-Kan allowed the exact input ratio to be calculated. After 3 days, spleens were recovered and passed through sieves (70 µm, Becton Dickinson) to produce a cell suspension in 3 ml LB. Homogenates were plated on selective media to determine the output ratio. The competitive index is defined as the output ratio (mutant/wt) divided by the input ratio (mutant/wt).

In-vitro CI was determined as described in Chiang *et al.*, Mol. Microbiol., 1998; 27: 797-805. Briefly, mixtures containing a mutant and the wild-type strains were inoculated into LB media supplemented with nalidixic acid at approximately $1x10^4$ cfu/ml. The cultures were grown overnight at 28°C and the mutant to wild-type ratios were determined by plating on media with and without selective marker (kanamycin).

The majority of the selected mutants with reduced output signals did not reveal significant reduction in *in vitro* growth properties and were confirmed to be attenuated (Table 1). Four mutants (1D9, 1D2, 4H9 and 3H10) revealed substantial (more than six times) reduction in CI. In all cases, the genes affected are related to LPS or LPS core biosynthesis. For example, an orthologue to a gene inactivated in 4H10 is located in an operon containing a number of other genes, such as *kdtB*, *waaA*, *rfaC*, *rfaD* and *rfaF*, all related to core biosyntheses. The insert in mutant 3H10 would also inactivate a gene encoding an LPS core-related glycosyltransferase. Inactivation of genes in other mutants of this class may have a dramatic effect on outer membrane stability due to an affect on LPS biosynthesis.

In vivo CI figures of less than 0.3 were demonstrated in 14 out of 20 cases, confirming attenuated properties of these mutants.

In vivo competition studies revealed significant attenuation of the 3F10 (PldA) derivative. The competitive index (CI=0.01655) obtained in the mixed infection experiment confirmed that the strain was severely attenuated. These data suggest that *PldA* is an essential virulence factor in the murine yersiniosis model of infection.

CLAIMS

1. A peptide encoded by a gene comprising any of the nucleotide sequences identified herein as SEQ ID NOS. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 57, 58 and 64, of *Yersinia pseudotuberculosis*, or a related molecule having at least 60% sequence similarity or identity at the peptide level in a Gram-negative bacterium, or a functional fragment thereof, for therapeutic or diagnostic use.

2. A peptide according to claim 1, wherein the sequence similarity or identity is at least 80%.

3. A peptide according to claim 1 or claim 2, wherein the sequence similarity or identity is at least 90%.

4. A peptide according to claim 1, comprising any of the amino acid sequences identified herein as SEQ ID NO. 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55 and 65.

5. A polynucleotide encoding a peptide according to any preceding claim, for therapeutic or diagnostic use.

6. A recombinant host genetically modified to express a peptide according to any of claims 1 to 4.

7. An attenuated microorganism comprising a mutation that disrupts the expression of the nucleotide sequence defined in claim 1 or that identified herein as SEQ ID NO. 59, 60, 61, 62 or 63, or homologue thereof.

8. A microorganism according to claim 7, wherein the mutation is insertional inactivation or a gene deletion.

9. A microorganism according to claim 7 or claim 8, wherein the microorganism is *Yersinia pseudotuberculosis* or *Yersinia pestis*.

10. A microorganism according to any of claims 7 to 9, comprising a second mutation in a second nucleotide sequence.

11. A microorganism according to any of claims 7 to 10, comprising a heterologous antigen, therapeutic peptide or nucleic acid.

12. A microorganism according to any of claims 7 to 11, for therapeutic or diagnostic use.

13. A vaccine comprising a peptide according to any of claims 1 to 4.

14. A vaccine comprising a microorganism according to any of claims 7 to 12.

15. An antibody raised against a peptide according to any of claims 1 to 4.

16. Use of a product according to any of claims 1 to 12, for the manufacture of a medicament for use in the treatment or prevention of a condition associated with infection by *Yersinia*.
17. Use according to claim 16, wherein the condition is tuberculosis.
18. Use according to claim 16 or claim 17, for veterinary treatment.
19. Use of a peptide, polynucleotide or microorganism, according to any of claims 1 to 12, in a screening assay for the identification of an antimicrobial drug.

SEQUENCE LISTING

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<120> Virulence Genes, Proteins, and Their Use

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Ala Ser Leu Leu Thr Asp Cys Leu Ala Ser Val Ala Trp Ala Asp Glu
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ata atc gta tta gac tca ggc agt gaa gat gaa aca cgg gca tta gct    144
Ile Ile Val Leu Asp Ser Gly Ser Glu Asp Glu Thr Arg Ala Leu Ala
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Ile Glu Ser Val Leu Leu Ala Pro Glu Glu Gly Ala Val Tyr Ser Cys
            100                 105                 110

tca cgc cgg aac ctc ttt tta ggg cgt ttt atg cgc cac agc ggc tgg      384
Ser Arg Arg Asn Leu Phe Leu Gly Arg Phe Met Arg His Ser Gly Trp
        115                 120                 125

tat cca gat agg gtg act cgg tta tat cct cat cac caa tat cgc tac      432
Tyr Pro Asp Arg Val Thr Arg Leu Tyr Pro His His Gln Tyr Arg Tyr
    130                 135                 140

aac gat aat tta gtc cat gaa tca ctc gat agc ggc tca gca aaa gtt      480
Asn Asp Asn Leu Val His Glu Ser Leu Asp Ser Gly Ser Ala Lys Val
145                 150                 155                 160

atc cca ctg gct ggt gat tta ttg cat ctg act tgc cgc gac ttt ttt      528
Ile Pro Leu Ala Gly Asp Leu Leu His Leu Thr Cys Arg Asp Phe Phe
                165                 170                 175

gcc ttt caa cgt aaa cag ctt agt tat gcc gaa gca tgg gcc atc caa      576
Ala Phe Gln Arg Lys Gln Leu Ser Tyr Ala Glu Ala Trp Ala Ile Gln
            180                 185                 190

cgt cat cag caa ggc aaa agt tgc agt tat ttt gcc att ctc agc cat      624
Arg His Gln Gln Gly Lys Ser Cys Ser Tyr Phe Ala Ile Leu Ser His
        195                 200                 205

act ctt ggg gca ttc agt aaa acg tgg tta tta cgt gct ggc ttc ctt      672
Thr Leu Gly Ala Phe Ser Lys Thr Trp Leu Leu Arg Ala Gly Phe Leu
    210                 215                 220

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225                 230                 235                 240

ttt aat aaa tat gct gct ctg tgg gca ttg agc cac cag tat cag aaa      768
Phe Asn Lys Tyr Ala Ala Leu Trp Ala Leu Ser His Gln Tyr Gln Lys
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Ile Ile Val Leu Asp Ser Gly Ser Glu Asp Glu Thr Arg Ala Leu Ala
        35                  40                  45

Gln Gln Phe Gly Ala Lys Val Tyr Ser Asn Ile Asn Trp Pro Gly Tyr
    50                  55                  60

Gly Lys Gln Arg Gln Leu Ala Gln Gln Tyr Ala Ser Gly Asp Tyr Ile
65                  70                  75                  80

Leu Met Leu Asp Ala Asp Glu Arg Val Thr Pro Glu Leu Lys Ile Ala
                85                  90                  95

Ile Glu Ser Val Leu Leu Ala Pro Glu Glu Gly Ala Val Tyr Ser Cys
            100                 105                 110

Ser Arg Arg Asn Leu Phe Leu Gly Arg Phe Met Arg His Ser Gly Trp
        115                 120                 125

Tyr Pro Asp Arg Val Thr Arg Leu Tyr Pro His His Gln Tyr Arg Tyr
    130                 135                 140

Asn Asp Asn Leu Val His Glu Ser Leu Asp Ser Gly Ser Ala Lys Val
145                 150                 155                 160

Ile Pro Leu Ala Gly Asp Leu Leu His Leu Thr Cys Arg Asp Phe Phe
                165                 170                 175

Ala Phe Gln Arg Lys Gln Leu Ser Tyr Ala Glu Ala Trp Ala Ile Gln
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Arg His Gln Gln Gly Lys Ser Cys Ser Tyr Phe Ala Ile Leu Ser His
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Thr Leu Gly Ala Phe Ser Lys Thr Trp Leu Leu Arg Ala Gly Phe Leu
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Gly Met Ile Ile Asn Lys Phe His Ser Gly Gln Val Asp Gly Lys Pro
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Tyr Phe Cys Ile Glu Ala Phe Lys Pro Ser Thr Thr Ile Thr Ala Cys
50 55 60

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gat cag gct atg tat tat tat aca acc ggt aag cgt atc aga gtt tat 288
Asp Gln Ala Met Tyr Tyr Tyr Thr Thr Gly Lys Arg Ile Arg Val Tyr
85 90 95

tac gct ccg gat gtc tgg act aat aat agt ttt gtg agg gca ctt aca 336
Tyr Ala Pro Asp Val Trp Thr Asn Asn Ser Phe Val Arg Ala Leu Thr

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            100                   105                   110

gca aat gct ctg gtt gga ttc tca acg tgt atc tcg gaa agt tcg tgc    384
Ala Asn Ala Leu Val Gly Phe Ser Thr Cys Ile Ser Glu Ser Ser Cys
        115                 120                 125

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Gly Met Ile Ile Asn Lys Phe His Ser Gly Gln Val Asp Gly Lys Pro
        35                  40                  45

Tyr Phe Cys Ile Glu Ala Phe Lys Pro Ser Thr Thr Ile Thr Ala Cys
    50                  55                  60

Ser Val Lys Asp Thr Ser Ile Trp Gly Ala Ser Tyr Asn Thr Leu Tyr
65                  70                  75                  80

Asp Gln Ala Met Tyr Tyr Tyr Thr Thr Gly Lys Arg Ile Arg Val Tyr
                85                  90                  95

Tyr Ala Pro Asp Val Trp Thr Asn Asn Ser Phe Val Arg Ala Leu Thr
            100                 105                 110

Ala Asn Ala Leu Val Gly Phe Ser Thr Cys Ile Ser Glu Ser Ser Cys
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1               5                   10                  15

atc tca aca tct tct ttg gct att aat tgc caa aga gcc tca acc ccc      96
Ile Ser Thr Ser Ser Leu Ala Ile Asn Cys Gln Arg Ala Ser Thr Pro
            20                  25                  30

gtc gag tat aca gtc tgc agc aat gag gat tta cac tgg ctg gat caa     144
Val Glu Tyr Thr Val Cys Ser Asn Glu Asp Leu His Trp Leu Asp Gln
        35                  40                  45

aca ttt aac agc att tat caa gtc tta ttg gtg aaa tac aat act gaa     192
Thr Phe Asn Ser Ile Tyr Gln Val Leu Leu Val Lys Tyr Asn Thr Glu
    50                  55                  60

atg gtt tat caa cag cgt caa aca tgg gaa aaa tcg ctg aac agt tgt     240
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                85                  90                  95

atg tct gat gtt gat aag aac ttt aac tgg gat ggg caa tgg tgg aat     336
Met Ser Asp Val Asp Lys Asn Phe Asn Trp Asp Gly Gln Trp Trp Asn
            100                 105                 110

atc act aaa ggt aat gac cgt ggt ggg gtt atc gaa att cat cga gtg     384
Ile Thr Lys Gly Asn Asp Arg Gly Gly Val Ile Glu Ile His Arg Val
        115                 120                 125

acc gag tgg gga ttt agt ctg gat agc cgt gca tgg tct ggt gag aat     432
Thr Glu Trp Gly Phe Ser Leu Asp Ser Arg Ala Trp Ser Gly Glu Asn
    130                 135                 140

atg ggt aat ttt cat gca gaa gcc cgt aaa aca gaa gga gta gcc gtt     480
Met Gly Asn Phe His Ala Glu Ala Arg Lys Thr Glu Gly Val Ala Val
145                 150                 155                 160
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gga aaa gat ggc tcg cta cag gtg cac agt aat ggc agt tgg ggg tgt     576
Gly Lys Asp Gly Ser Leu Gln Val His Ser Asn Gly Ser Trp Gly Cys
            180                 185                 190

cgt atc tcc atg ccg aaa gat gtt ttc atc gac ggg caa tat gtg cgt     624
Arg Ile Ser Met Pro Lys Asp Val Phe Ile Asp Gly Gln Tyr Val Arg
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gct gaa aaa gat ccc cgt aag gcc cca acg tta tta tct att ggt att     672
Ala Glu Lys Asp Pro Arg Lys Ala Pro Thr Leu Leu Ser Ile Gly Ile
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gat ttg gat aac cag gga gcc aaa gtg tta tct acc tgg gtg cgg ggg     816
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65                  70                  75                  80

Thr Ser Asp Ser Cys Ile Gln Arg Ala Tyr Leu Gln Gly Ile Ala Leu
                85                  90                  95

Met Ser Asp Val Asp Lys Asn Phe Asn Trp Asp Gly Gln Trp Trp Asn
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Ile Thr Lys Gly Asn Asp Arg Gly Gly Val Ile Glu Ile His Arg Val
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Val Asp Val Ile Glu Asn Thr Ala Asn Cys Arg Leu Leu Leu Ile Pro
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Gly Lys Asp Gly Ser Leu Gln Val His Ser Asn Gly Ser Trp Gly Cys
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Arg Ile Ser Met Pro Lys Asp Val Phe Ile Asp Gly Gln Tyr Val Arg
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Tyr Trp Ala Ala Tyr Val Ala Pro Asp Lys Lys Gly Gln Leu Gln Ile
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35 40 45

acc gca tcc tgc gaa tca aaa atc acc tat att gat ggt gat cag ggt 192
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                85                  90                  95

cca gaa gag tac aaa acg ttc aaa acc aca gtg acc cga cat acc atg     336
Pro Glu Glu Tyr Lys Thr Phe Lys Thr Thr Val Thr Arg His Thr Met
            100                 105                 110

atc cac gag cag atc acc cgt ctg ttc cat ggt ttc cgc cgc gat tca     384
Ile His Glu Gln Ile Thr Arg Leu Phe His Gly Phe Arg Arg Asp Ser
        115                 120                 125

cat ccg atg gcc gtg cta tgt ggg gtt act ggt gcg cta gcc gcc ttc     432
His Pro Met Ala Val Leu Cys Gly Val Thr Gly Ala Leu Ala Ala Phe
    130                 135                 140

tac cat gat gct ctg gat gtt aat aac gag cgc cat cgt gaa att acc     480
Tyr His Asp Ala Leu Asp Val Asn Asn Glu Arg His Arg Glu Ile Thr
145                 150                 155                 160

gcc ttc cgt ctg ttg tct aaa atg ccg act gtc gca gcg atg tgt tat     528
Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Val Ala Ala Met Cys Tyr
                165                 170                 175

aaa tat tca ctg ggt caa ccg ttt gtt tat cca cgt aac gat ctg tcc     576
Lys Tyr Ser Leu Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu Ser
            180                 185                 190

tac gcg ggt aac ttc cta cac atg atg ttc tct acg cca tgt gag aaa     624
Tyr Ala Gly Asn Phe Leu His Met Met Phe Ser Thr Pro Cys Glu Lys
        195                 200                 205

tat gaa gtt aac cca gta ctg gaa cgc gct atg gat cgt att ctc atc     672
Tyr Glu Val Asn Pro Val Leu Glu Arg Ala Met Asp Arg Ile Leu Ile
    210                 215                 220

ctg cac gca gat cac gaa cag aac gcg tca aca tcg acc gtc cgt act     720
Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg Thr
225                 230                 235                 240

gcc ggc tct tct ggc gct aac ccg ttt gcc tgt atc gcc gcg ggg atc     768
Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly Ile
                245                 250                 255

gca tcc ctg tgg ggc cct gcg cac ggt ggt gcc aat gaa gcc tgc ctg     816
Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Cys Leu
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Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe Gly
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cac cgt gtc tat aaa aac tat gac cct cgt gcc acc gtc atg cgt gaa 960
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20 25 30

Thr Leu Gly Ser Lys Gly Tyr Phe Thr Phe Asp Pro Gly Phe Thr Ser
35 40 45

Thr Ala Ser Cys Glu Ser Lys Ile Thr Tyr Ile Asp Gly Asp Gln Gly
50 55 60

Ile Leu Leu His Arg Gly Phe Pro Ile Ala Gln Leu Ala Lys Asp Ser
65 70 75 80

Thr Tyr Leu Glu Val Cys Tyr Ile Leu Leu Tyr Gly Glu Thr Pro Thr
85 90 95

Pro Glu Glu Tyr Lys Thr Phe Lys Thr Thr Val Thr Arg His Thr Met
100 105 110

Ile His Glu Gln Ile Thr Arg Leu Phe His Gly Phe Arg Arg Asp Ser
115 120 125

His Pro Met Ala Val Leu Cys Gly Val Thr Gly Ala Leu Ala Ala Phe
130 135 140

Tyr His Asp Ala Leu Asp Val Asn Asn Glu Arg His Arg Glu Ile Thr
145 150 155 160

Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Val Ala Ala Met Cys Tyr
165 170 175

Lys Tyr Ser Leu Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu Ser
180 185 190

Tyr Ala Gly Asn Phe Leu His Met Met Phe Ser Thr Pro Cys Glu Lys
195 200 205

Tyr Glu Val Asn Pro Val Leu Glu Arg Ala Met Asp Arg Ile Leu Ile
210 215 220

Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg Thr
225 230 235 240

Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly Ile
245 250 255

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Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Cys Leu
            260                 265                 270

Lys Met Leu Glu Glu Ile Lys Thr Val Glu His Ile Pro Glu Phe Ile
        275                 280                 285

Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe Gly
    290                 295                 300

His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg Glu
305                 310                 315                 320

Thr Cys His Glu Val Leu Glu Glu Leu Lys Leu Asn Asn Ser Leu Leu
                325                 330                 335

Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr Phe
            340                 345                 350

Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile Ile
        355                 360                 365

Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe Ala
    370                 375                 380

Ile Ala Arg Thr Ile Gly Trp Ile Ala His Trp Asn Glu Met His Asn
385                 390                 395                 400

Asp Gly Ile Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr Thr
                405                 410                 415

Glu Arg Asp Phe Gln Ser Gln Leu Lys Lys
            420                 425



<210> 9
<211> 930
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(930)

<400> 9
atg cca caa gtt aat aac ata tcg aca aac aat ata cac tca gcc ggc      48
Met Pro Gln Val Asn Asn Ile Ser Thr Asn Asn Ile His Ser Ala Gly
```

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1               5                   10                  15

ttt aac aac tca aat tca att caa aaa tat act gga gca gtc tca tct   96
Phe Asn Asn Ser Asn Ser Ile Gln Lys Tyr Thr Gly Ala Val Ser Ser
            20                  25                  30

ata agt gat gat tta cgt att aat aat gaa aag tgc aag agt gac ata   144
Ile Ser Asp Asp Leu Arg Ile Asn Asn Glu Lys Cys Lys Ser Asp Ile
        35                  40                  45

gga act ata agt ggt gat ata aaa att aat cgc cat tct gca gtc tac   192
Gly Thr Ile Ser Gly Asp Ile Lys Ile Asn Arg His Ser Ala Val Tyr
    50                  55                  60

ggt aat gtg aat tca gtc agt ggc gat att act gta aaa aat tct ata   240
Gly Asn Val Asn Ser Val Ser Gly Asp Ile Thr Val Lys Asn Ser Ile
65                  70                  75                  80

gta gat aaa gac atc acc aca gta agt ggt gat gtt aac gcg gtg aat   288
Val Asp Lys Asp Ile Thr Thr Val Ser Gly Asp Val Asn Ala Val Asn
                85                  90                  95

tcg act ata gga aaa aat ata aaa aca gtc agt ggt tcg att gag gtg   336
Ser Thr Ile Gly Lys Asn Ile Lys Thr Val Ser Gly Ser Ile Glu Val
            100                 105                 110

gaa caa tca act gta agc ggc aat ttg gaa aca aca agt ggt ggg ata   384
Glu Gln Ser Thr Val Ser Gly Asn Leu Glu Thr Thr Ser Gly Gly Ile
        115                 120                 125

gat ata gat aca aca aaa att aac ggt aat gtg cat acg aca agt ggt   432
Asp Ile Asp Thr Thr Lys Ile Asn Gly Asn Val His Thr Thr Ser Gly
    130                 135                 140

tca att tcg atg aac gat tca act att gat ggt agc gta aca tgt aag   480
Ser Ile Ser Met Asn Asp Ser Thr Ile Asp Gly Ser Val Thr Cys Lys
145                 150                 155                 160

gcg ggg tct gta aca att gtc aat tca aca att aaa gaa agc ctt aat   528
Ala Gly Ser Val Thr Ile Val Asn Ser Thr Ile Lys Glu Ser Leu Asn
                165                 170                 175

gta acc agt gag aaa ata att gtt ggt aca gca tct tgt att gga aaa   576
Val Thr Ser Glu Lys Ile Ile Val Gly Thr Ala Ser Cys Ile Gly Lys
            180                 185                 190

att aac att tcc ccc cct gaa tct gta aat ttt aac atc atg aat ttt   624
Ile Asn Ile Ser Pro Pro Glu Ser Val Asn Phe Asn Ile Met Asn Phe
```

195 200 205

ggg aac gat agt ata gtg atg gga atg agg aat ttt tgt att tca gga 672
Gly Asn Asp Ser Ile Val Met Gly Met Arg Asn Phe Cys Ile Ser Gly
210 215 220

gag gta aat ttt acc att act aat ggt aaa gta ttt gtt aat gaa caa 720
Glu Val Asn Phe Thr Ile Thr Asn Gly Lys Val Phe Val Asn Glu Gln
225 230 235 240

agg gtc ggc cat aca gct tcg caa tca act tcg aaa aaa gta gaa gaa 768
Arg Val Gly His Thr Ala Ser Gln Ser Thr Ser Lys Lys Val Glu Glu
245 250 255

gtt act att aat atc gcg aaa aat gcc agt gtt aat gat att gtt ttt 816
Val Thr Ile Asn Ile Ala Lys Asn Ala Ser Val Asn Asp Ile Val Phe
260 265 270

tat act aaa aag tgc cat atc att tta gaa gga aat gct aaa tat aac 864
Tyr Thr Lys Lys Cys His Ile Ile Leu Glu Gly Asn Ala Lys Tyr Asn
275 280 285

gga gaa aaa aag gat ggc atg caa ttc acc cat gtt aac gca ccg aaa 912
Gly Glu Lys Lys Asp Gly Met Gln Phe Thr His Val Asn Ala Pro Lys
290 295 300

agt cat gct tat gcg taa 930
Ser His Ala Tyr Ala
305 310

<210> 10
<211> 309
<212> PRT
<213> Yersinia pestis

<400> 10
Met Pro Gln Val Asn Asn Ile Ser Thr Asn Asn Ile His Ser Ala Gly
1 5 10 15

Phe Asn Asn Ser Asn Ser Ile Gln Lys Tyr Thr Gly Ala Val Ser Ser
20 25 30

Ile Ser Asp Asp Leu Arg Ile Asn Asn Glu Lys Cys Lys Ser Asp Ile
35 40 45

Gly Thr Ile Ser Gly Asp Ile Lys Ile Asn Arg His Ser Ala Val Tyr
50 55 60

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Gly Asn Val Asn Ser Val Ser Gly Asp Ile Thr Val Lys Asn Ser Ile
65                  70                  75                  80

Val Asp Lys Asp Ile Thr Thr Val Ser Gly Asp Val Asn Ala Val Asn
                85                  90                  95

Ser Thr Ile Gly Lys Asn Ile Lys Thr Val Ser Gly Ser Ile Glu Val
            100                 105                 110

Glu Gln Ser Thr Val Ser Gly Asn Leu Glu Thr Thr Ser Gly Gly Ile
        115                 120                 125

Asp Ile Asp Thr Thr Lys Ile Asn Gly Asn Val His Thr Thr Ser Gly
    130                 135                 140

Ser Ile Ser Met Asn Asp Ser Thr Ile Asp Gly Ser Val Thr Cys Lys
145                 150                 155                 160

Ala Gly Ser Val Thr Ile Val Asn Ser Thr Ile Lys Glu Ser Leu Asn
                165                 170                 175

Val Thr Ser Glu Lys Ile Ile Val Gly Thr Ala Ser Cys Ile Gly Lys
            180                 185                 190

Ile Asn Ile Ser Pro Pro Glu Ser Val Asn Phe Asn Ile Met Asn Phe
        195                 200                 205

Gly Asn Asp Ser Ile Val Met Gly Met Arg Asn Phe Cys Ile Ser Gly
    210                 215                 220

Glu Val Asn Phe Thr Ile Thr Asn Gly Lys Val Phe Val Asn Glu Gln
225                 230                 235                 240

Arg Val Gly His Thr Ala Ser Gln Ser Thr Ser Lys Lys Val Glu Glu
                245                 250                 255

Val Thr Ile Asn Ile Ala Lys Asn Ala Ser Val Asn Asp Ile Val Phe
            260                 265                 270

Tyr Thr Lys Lys Cys His Ile Ile Leu Glu Gly Asn Ala Lys Tyr Asn
        275                 280                 285

Gly Glu Lys Lys Asp Gly Met Gln Phe Thr His Val Asn Ala Pro Lys
    290                 295                 300

Ser His Ala Tyr Ala
305
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<210> 11
<211> 474
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(474)

<400> 11
atg atc aac aac gat gtg ctc cgc agt gtt cgc tat atg ctt aac gtt      48
Met Ile Asn Asn Asp Val Leu Arg Ser Val Arg Tyr Met Leu Asn Val
1               5                   10                  15

aac gat acc aaa ata gca gaa atc att aag ctg gct gat ttt gaa gtg      96
Asn Asp Thr Lys Ile Ala Glu Ile Ile Lys Leu Ala Asp Phe Glu Val
            20                  25                  30

aac aac gca gat gtc gtt aat ttt ctt aaa aaa gaa gac gaa gcc ggt      144
Asn Asn Ala Asp Val Val Asn Phe Leu Lys Lys Glu Asp Glu Ala Gly
        35                  40                  45

tat cag gat tgc cct gat ctg gtg atg gcg cat ttt ctg aat ggt ttg      192
Tyr Gln Asp Cys Pro Asp Leu Val Met Ala His Phe Leu Asn Gly Leu
    50                  55                  60

att ttc ttt aga cgt ggt aaa gat gat aag ttc cct gca cct gcg gta      240
Ile Phe Phe Arg Arg Gly Lys Asp Asp Lys Phe Pro Ala Pro Ala Val
65                  70                  75                  80

gag gcg gtt atc acc aac aat att gtg ttg aaa aaa ctg cgt gtc gca      288
Glu Ala Val Ile Thr Asn Asn Ile Val Leu Lys Lys Leu Arg Val Ala
                85                  90                  95

ttc gaa ttg aaa gac acc gat atg cat gat gtt ttt aat gcc gtt gaa      336
Phe Glu Leu Lys Asp Thr Asp Met His Asp Val Phe Asn Ala Val Glu
            100                 105                 110

ttc cca gtc tct aag cct gag tta aat gct ctg ttc cgt aaa gag ggc      384
Phe Pro Val Ser Lys Pro Glu Leu Asn Ala Leu Phe Arg Lys Glu Gly
        115                 120                 125

agc aaa aac ttc cgc cct tgt ggt gat cag gtt tta cgt tat ttt ctg      432
Ser Lys Asn Phe Arg Pro Cys Gly Asp Gln Val Leu Arg Tyr Phe Leu
    130                 135                 140
```

aag ggc ctg aca ctg cgt att cgt ggc gct aaa aaa gcc tag 474
Lys Gly Leu Thr Leu Arg Ile Arg Gly Ala Lys Lys Ala
145 150 155

<210> 12
<211> 157
<212> PRT
<213> Yersinia pestis

<400> 12
Met Ile Asn Asn Asp Val Leu Arg Ser Val Arg Tyr Met Leu Asn Val
1 5 10 15

Asn Asp Thr Lys Ile Ala Glu Ile Ile Lys Leu Ala Asp Phe Glu Val
20 25 30

Asn Asn Ala Asp Val Val Asn Phe Leu Lys Lys Glu Asp Glu Ala Gly
35 40 45

Tyr Gln Asp Cys Pro Asp Leu Val Met Ala His Phe Leu Asn Gly Leu
50 55 60

Ile Phe Phe Arg Arg Gly Lys Asp Asp Lys Phe Pro Ala Pro Ala Val
65 70 75 80

Glu Ala Val Ile Thr Asn Asn Ile Val Leu Lys Lys Leu Arg Val Ala
85 90 95

Phe Glu Leu Lys Asp Thr Asp Met His Asp Val Phe Asn Ala Val Glu
100 105 110

Phe Pro Val Ser Lys Pro Glu Leu Asn Ala Leu Phe Arg Lys Glu Gly
115 120 125

Ser Lys Asn Phe Arg Pro Cys Gly Asp Gln Val Leu Arg Tyr Phe Leu
130 135 140

Lys Gly Leu Thr Leu Arg Ile Arg Gly Ala Lys Lys Ala
145 150 155

<210> 13
<211> 675
<212> DNA
<213> Yersinia pestis

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<220>
<221> CDS
<222> (1)..(675)

<400> 13
atg aat gaa aat tgg aat tgg tct tta gta gac aaa gtt gtt tac att      48
Met Asn Glu Asn Trp Asn Trp Ser Leu Val Asp Lys Val Val Tyr Ile
1               5                   10                  15

aat ttg aag gaa cgt acg gat aga aat gag cac atc aaa aaa gaa ctg      96
Asn Leu Lys Glu Arg Thr Asp Arg Asn Glu His Ile Lys Lys Glu Leu
            20                  25                  30

gaa aaa gtg tgc ttt cca cct gaa aaa ata atc cgc ttt gag gca ata     144
Glu Lys Val Cys Phe Pro Pro Glu Lys Ile Ile Arg Phe Glu Ala Ile
        35                  40                  45

aga gca ggg tca ggt ttt atc ggt tgc gca aaa tca cat ctt gca gta     192
Arg Ala Gly Ser Gly Phe Ile Gly Cys Ala Lys Ser His Leu Ala Val
    50                  55                  60

tta aaa atg gcg caa gag aat aat tgg aga aat att ttg ata ctt gaa     240
Leu Lys Met Ala Gln Glu Asn Asn Trp Arg Asn Ile Leu Ile Leu Glu
65                  70                  75                  80

gac gat atg gtc ttc gaa gat gat gat gaa aca att atc cgg aca aac     288
Asp Asp Met Val Phe Glu Asp Asp Asp Glu Thr Ile Ile Arg Thr Asn
                85                  90                  95

aat ttt ctc tct aaa ctg aat aat att cat tgg gat gct gca ttt tta     336
Asn Phe Leu Ser Lys Leu Asn Asn Ile His Trp Asp Ala Ala Phe Leu
            100                 105                 110

tcc gcc agc tat tat atc gtt aac gct att gat gat aat ttt ttt aaa     384
Ser Ala Ser Tyr Tyr Ile Val Asn Ala Ile Asp Asp Asn Phe Phe Lys
        115                 120                 125

gtc aat ttc gcc tat ctg gct aac agc tat ctg gtc aat aat cat tat     432
Val Asn Phe Ala Tyr Leu Ala Asn Ser Tyr Leu Val Asn Asn His Tyr
    130                 135                 140

tat gaa aaa tta atc aat aac tac acg gag tct gtt cag cga tta aca     480
Tyr Glu Lys Leu Ile Asn Asn Tyr Thr Glu Ser Val Gln Arg Leu Thr
145                 150                 155                 160

aat ggc gag tca tcg tca gag tac ggg ttg gat tct aac tgg ttg aaa     528
Asn Gly Glu Ser Ser Ser Glu Tyr Gly Leu Asp Ser Asn Trp Leu Lys
```

165 170 175

ata atg aaa ata gac aac tgg tac gga att tac ccg gtt att ggc tat 576
Ile Met Lys Ile Asp Asn Trp Tyr Gly Ile Tyr Pro Val Ile Gly Tyr
180 185 190

cag cgt acc gat atc agt gat att gaa tat aaa gag atc gat cgc aca 624
Gln Arg Thr Asp Ile Ser Asp Ile Glu Tyr Lys Glu Ile Asp Arg Thr
195 200 205

cac cag ttc acc cga aca ttc gat aag atg aaa gca tac ggt tca aaa 672
His Gln Phe Thr Arg Thr Phe Asp Lys Met Lys Ala Tyr Gly Ser Lys
210 215 220

taa 675

225

<210> 14
<211> 224
<212> PRT
<213> Yersinia pestis

<400> 14
Met Asn Glu Asn Trp Asn Trp Ser Leu Val Asp Lys Val Val Tyr Ile
1 5 10 15

Asn Leu Lys Glu Arg Thr Asp Arg Asn Glu His Ile Lys Lys Glu Leu
20 25 30

Glu Lys Val Cys Phe Pro Pro Glu Lys Ile Ile Arg Phe Glu Ala Ile
35 40 45

Arg Ala Gly Ser Gly Phe Ile Gly Cys Ala Lys Ser His Leu Ala Val
50 55 60

Leu Lys Met Ala Gln Glu Asn Asn Trp Arg Asn Ile Leu Ile Leu Glu
65 70 75 80

Asp Asp Met Val Phe Glu Asp Asp Asp Glu Thr Ile Ile Arg Thr Asn
85 90 95

Asn Phe Leu Ser Lys Leu Asn Asn Ile His Trp Asp Ala Ala Phe Leu
100 105 110

Ser Ala Ser Tyr Tyr Ile Val Asn Ala Ile Asp Asp Asn Phe Phe Lys
115 120 125

Val Asn Phe Ala Tyr Leu Ala Asn Ser Tyr Leu Val Asn Asn His Tyr
130 135 140

Tyr Glu Lys Leu Ile Asn Asn Tyr Thr Glu Ser Val Gln Arg Leu Thr
145 150 155 160

Asn Gly Glu Ser Ser Ser Glu Tyr Gly Leu Asp Ser Asn Trp Leu Lys
165 170 175

Ile Met Lys Ile Asp Asn Trp Tyr Gly Ile Tyr Pro Val Ile Gly Tyr
180 185 190

Gln Arg Thr Asp Ile Ser Asp Ile Glu Tyr Lys Glu Ile Asp Arg Thr
195 200 205

His Gln Phe Thr Arg Thr Phe Asp Lys Met Lys Ala Tyr Gly Ser Lys
210 215 220

<210> 15
<211> 1659
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(1659)

<400> 15
ttg agc ttc gct cat gca cag aca ttg ccc gat gtc tat tca gtg gtt 48
Leu Ser Phe Ala His Ala Gln Thr Leu Pro Asp Val Tyr Ser Val Val
1 5 10 15

gaa cga aaa ctg gaa aat gcc cta ccg ctg gcg gaa cac ccc cat tat 96
Glu Arg Lys Leu Glu Asn Ala Leu Pro Leu Ala Glu His Pro His Tyr
20 25 30

gat gct cag gcc cct tat ttc gaa ctg cac cga gaa atc ctg atg ttt 144
Asp Ala Gln Ala Pro Tyr Phe Glu Leu His Arg Glu Ile Leu Met Phe
35 40 45

agc tca cca gaa cga gcc aat acg cta tta aag aaa ctt gat ttc agt 192
Ser Ser Pro Glu Arg Ala Asn Thr Leu Leu Lys Lys Leu Asp Phe Ser
50 55 60

tcg aaa gag gca atg tta tca ctg aat att tct gct gac tgg att gcg 240

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Ser Lys Glu Ala Met Leu Ser Leu Asn Ile Ser Ala Asp Trp Ile Ala
 65                  70                  75                  80

gga aca ggt aat cca gac aaa gca atg gta ttt tta tca cag att gga      288
Gly Thr Gly Asn Pro Asp Lys Ala Met Val Phe Leu Ser Gln Ile Gly
                 85                  90                  95

ctc gag aaa ccg agc tca ttc tca gca tac aag aat tat gtt gat gcc      336
Leu Glu Lys Pro Ser Ser Phe Ser Ala Tyr Lys Asn Tyr Val Asp Ala
            100                 105                 110

tgg att gaa aag aaa cag cct gaa tct gcg tta aag tta ctt atg ctg      384
Trp Ile Glu Lys Lys Gln Pro Glu Ser Ala Leu Lys Leu Leu Met Leu
        115                 120                 125

gat aac agt gca agg aac tat tat ctt ccc gct gtt tta gac gct tat      432
Asp Asn Ser Ala Arg Asn Tyr Tyr Leu Pro Ala Val Leu Asp Ala Tyr
    130                 135                 140

cga gat acg cca gat caa gcg gtg act att tat aaa gat att tat ggc      480
Arg Asp Thr Pro Asp Gln Ala Val Thr Ile Tyr Lys Asp Ile Tyr Gly
145                 150                 155                 160

gac aac ata ata gaa ccg acc aat caa tta agg atg ctg ctt gct att      528
Asp Asn Ile Ile Glu Pro Thr Asn Gln Leu Arg Met Leu Leu Ala Ile
                165                 170                 175

gca gaa aat tat cgt gtc aac ggt gcc ccc aaa aac acc ctt att tat      576
Ala Glu Asn Tyr Arg Val Asn Gly Ala Pro Lys Asn Thr Leu Ile Tyr
            180                 185                 190

acc gat aaa gca cag gta atg ttt atc gac gtg ctc aaa aag aag aag      624
Thr Asp Lys Ala Gln Val Met Phe Ile Asp Val Leu Lys Lys Lys Lys
        195                 200                 205

aac aat gaa att cat ttt tat aaa gat tac ttg aat ttg atc aat cta      672
Asn Asn Glu Ile His Phe Tyr Lys Asp Tyr Leu Asn Leu Ile Asn Leu
    210                 215                 220

tat tca ttt gca ggt aat aag caa caa gca tta ata tta tca gaa cag      720
Tyr Ser Phe Ala Gly Asn Lys Gln Gln Ala Leu Ile Leu Ser Glu Gln
225                 230                 235                 240

cta ctc agg gcg gcc gga gat aaa ggt acc tat tat gat ttg gca tta      768
Leu Leu Arg Ala Ala Gly Asp Lys Gly Thr Tyr Tyr Asp Leu Ala Leu
                245                 250                 255

tcc ggg atc atg gca ttt tac cat gct aat ggt ttc act gaa gaa tac      816
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Ser Gly Ile Met Ala Phe Tyr His Ala Asn Gly Phe Thr Glu Glu Tyr
            260                 265                 270

aat gca tta att gca acc agc att gcc act aca gat aag tcc ttt agc     864
Asn Ala Leu Ile Ala Thr Ser Ile Ala Thr Thr Asp Lys Ser Phe Ser
        275                 280                 285

ttt gct ccc aag cct ata gaa gaa ata aag ctt atc cgg ttg ttg aat     912
Phe Ala Pro Lys Pro Ile Glu Glu Ile Lys Leu Ile Arg Leu Leu Asn
    290                 295                 300

gcc act aac gaa acc ggc cta att aaa gag cgt att gat aag ctg atg     960
Ala Thr Asn Glu Thr Gly Leu Ile Lys Glu Arg Ile Asp Lys Leu Met
305                 310                 315                 320

atc tca cca gaa tat gcc tgt tat gac gat aga tat tgc tat gaa tat    1008
Ile Ser Pro Glu Tyr Ala Cys Tyr Asp Asp Arg Tyr Cys Tyr Glu Tyr
                325                 330                 335

aaa ata gat tcg ctt aat ttt cta tat tta agc aaa tct gat gca tta    1056
Lys Ile Asp Ser Leu Asn Phe Leu Tyr Leu Ser Lys Ser Asp Ala Leu
            340                 345                 350

gct gat aaa tat tta aac att att att gaa gaa tca caa aat caa aaa    1104
Ala Asp Lys Tyr Leu Asn Ile Ile Ile Glu Glu Ser Gln Asn Gln Lys
        355                 360                 365

ttc aat cca tgg gaa acg gta act aaa tcc atc gtt aaa aaa tta gtt    1152
Phe Asn Pro Trp Glu Thr Val Thr Lys Ser Ile Val Lys Lys Leu Val
    370                 375                 380

gat att gga cgt atc gcc gaa gct aag aag ttg gct gca gat gca gag    1200
Asp Ile Gly Arg Ile Ala Glu Ala Lys Lys Leu Ala Ala Asp Ala Glu
385                 390                 395                 400

gtt att tat ctc tca cag cta aaa gac tct ccg ccc aaa gaa gtc gaa    1248
Val Ile Tyr Leu Ser Gln Leu Lys Asp Ser Pro Pro Lys Glu Val Glu
                405                 410                 415

aga aat tat agg gat ctt gct gaa atg tat ggt ttt gca ggc gat gtc    1296
Arg Asn Tyr Arg Asp Leu Ala Glu Met Tyr Gly Phe Ala Gly Asp Val
            420                 425                 430

gtc agc gct gaa cga ata ctt aat aag cat gtc acc acc gcc caa aat    1344
Val Ser Ala Glu Arg Ile Leu Asn Lys His Val Thr Thr Ala Gln Asn
        435                 440                 445

tac ttt att acc gat ctg ttt ata aaa aat aaa cag tgg gat gaa gcc    1392
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Tyr Phe Ile Thr Asp Leu Phe Ile Lys Asn Lys Gln Trp Asp Glu Ala
    450                 455                 460

aga gcg cgt gtt gtg aaa gat acc ggt ctt tct gga caa aac ctg acg    1440
Arg Ala Arg Val Val Lys Asp Thr Gly Leu Ser Gly Gln Asn Leu Thr
465                 470                 475                 480

tta ttg caa aat att tgt gct acc aat aca cct gaa tgc atg caa cat    1488
Leu Leu Gln Asn Ile Cys Ala Thr Asn Thr Pro Glu Cys Met Gln His
                485                 490                 495

atc acg ttc aca ctt aaa tca atg tta aca cgt gaa tcc att acc gca    1536
Ile Thr Phe Thr Leu Lys Ser Met Leu Thr Arg Glu Ser Ile Thr Ala
            500                 505                 510

gaa gat gca tca ggg aat caa caa ctc tac cag ttg ggg atc atc tac    1584
Glu Asp Ala Ser Gly Asn Gln Gln Leu Tyr Gln Leu Gly Ile Ile Tyr
        515                 520                 525

cac tct ctt ggg ata aag ccg acc gag gaa caa cag ctt ctc att caa    1632
His Ser Leu Gly Ile Lys Pro Thr Glu Glu Gln Gln Leu Leu Ile Gln
    530                 535                 540

aaa tta tat gat aat gcg gcg gcc taa                                1659
Lys Leu Tyr Asp Asn Ala Ala Ala
545                 550


<210> 16
<211> 552
<212> PRT
<213> Yersinia pestis

<400> 16
Leu Ser Phe Ala His Ala Gln Thr Leu Pro Asp Val Tyr Ser Val Val
1               5                   10                  15

Glu Arg Lys Leu Glu Asn Ala Leu Pro Leu Ala Glu His Pro His Tyr
            20                  25                  30

Asp Ala Gln Ala Pro Tyr Phe Glu Leu His Arg Glu Ile Leu Met Phe
        35                  40                  45

Ser Ser Pro Glu Arg Ala Asn Thr Leu Leu Lys Lys Leu Asp Phe Ser
    50                  55                  60

Ser Lys Glu Ala Met Leu Ser Leu Asn Ile Ser Ala Asp Trp Ile Ala
65                  70                  75                  80
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Gly Thr Gly Asn Pro Asp Lys Ala Met Val Phe Leu Ser Gln Ile Gly
                85                  90                  95

Leu Glu Lys Pro Ser Ser Phe Ser Ala Tyr Lys Asn Tyr Val Asp Ala
            100                 105                 110

Trp Ile Glu Lys Lys Gln Pro Glu Ser Ala Leu Lys Leu Leu Met Leu
        115                 120                 125

Asp Asn Ser Ala Arg Asn Tyr Tyr Leu Pro Ala Val Leu Asp Ala Tyr
    130                 135                 140

Arg Asp Thr Pro Asp Gln Ala Val Thr Ile Tyr Lys Asp Ile Tyr Gly
145                 150                 155                 160

Asp Asn Ile Ile Glu Pro Thr Asn Gln Leu Arg Met Leu Leu Ala Ile
                165                 170                 175

Ala Glu Asn Tyr Arg Val Asn Gly Ala Pro Lys Asn Thr Leu Ile Tyr
            180                 185                 190

Thr Asp Lys Ala Gln Val Met Phe Ile Asp Val Leu Lys Lys Lys Lys
        195                 200                 205

Asn Asn Glu Ile His Phe Tyr Lys Asp Tyr Leu Asn Leu Ile Asn Leu
    210                 215                 220

Tyr Ser Phe Ala Gly Asn Lys Gln Gln Ala Leu Ile Leu Ser Glu Gln
225                 230                 235                 240

Leu Leu Arg Ala Ala Gly Asp Lys Gly Thr Tyr Tyr Asp Leu Ala Leu
                245                 250                 255

Ser Gly Ile Met Ala Phe Tyr His Ala Asn Gly Phe Thr Glu Glu Tyr
            260                 265                 270

Asn Ala Leu Ile Ala Thr Ser Ile Ala Thr Thr Asp Lys Ser Phe Ser
        275                 280                 285

Phe Ala Pro Lys Pro Ile Glu Glu Ile Lys Leu Ile Arg Leu Leu Asn
    290                 295                 300

Ala Thr Asn Glu Thr Gly Leu Ile Lys Glu Arg Ile Asp Lys Leu Met
305                 310                 315                 320

Ile Ser Pro Glu Tyr Ala Cys Tyr Asp Asp Arg Tyr Cys Tyr Glu Tyr
                325                 330                 335
```

```
Lys Ile Asp Ser Leu Asn Phe Leu Tyr Leu Ser Lys Ser Asp Ala Leu
            340                 345                 350

Ala Asp Lys Tyr Leu Asn Ile Ile Ile Glu Glu Ser Gln Asn Gln Lys
        355                 360                 365

Phe Asn Pro Trp Glu Thr Val Thr Lys Ser Ile Val Lys Lys Leu Val
    370                 375                 380

Asp Ile Gly Arg Ile Ala Glu Ala Lys Lys Leu Ala Ala Asp Ala Glu
385                 390                 395                 400

Val Ile Tyr Leu Ser Gln Leu Lys Asp Ser Pro Pro Lys Glu Val Glu
                405                 410                 415

Arg Asn Tyr Arg Asp Leu Ala Glu Met Tyr Gly Phe Ala Gly Asp Val
            420                 425                 430

Val Ser Ala Glu Arg Ile Leu Asn Lys His Val Thr Thr Ala Gln Asn
        435                 440                 445

Tyr Phe Ile Thr Asp Leu Phe Ile Lys Asn Lys Gln Trp Asp Glu Ala
    450                 455                 460

Arg Ala Arg Val Val Lys Asp Thr Gly Leu Ser Gly Gln Asn Leu Thr
465                 470                 475                 480

Leu Leu Gln Asn Ile Cys Ala Thr Asn Thr Pro Glu Cys Met Gln His
                485                 490                 495

Ile Thr Phe Thr Leu Lys Ser Met Leu Thr Arg Glu Ser Ile Thr Ala
            500                 505                 510

Glu Asp Ala Ser Gly Asn Gln Gln Leu Tyr Gln Leu Gly Ile Ile Tyr
        515                 520                 525

His Ser Leu Gly Ile Lys Pro Thr Glu Glu Gln Gln Leu Leu Ile Gln
    530                 535                 540

Lys Leu Tyr Asp Asn Ala Ala Ala
545                 550
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<210> 17
<211> 951
<212> DNA

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<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(951)

<400> 17
atg ctc cta aat aat att acg cca gtg aat aaa tca ctg aca cta caa     48
Met Leu Leu Asn Asn Ile Thr Pro Val Asn Lys Ser Leu Thr Leu Gln
  1               5                  10                  15

gat tta tta gga att ttg agt cac tca tcg gca att tcc aat gtg gca     96
Asp Leu Leu Gly Ile Leu Ser His Ser Ser Ala Ile Ser Asn Val Ala
             20                  25                  30

aat ggg att tat gtg gaa agc gaa atc ctt gaa gta ggt tca tgg ctt    144
Asn Gly Ile Tyr Val Glu Ser Glu Ile Leu Glu Val Gly Ser Trp Leu
         35                  40                  45

tca gcc tac gcg gct aat aaa gat gaa att ttt tcg cag atc att acc    192
Ser Ala Tyr Ala Ala Asn Lys Asp Glu Ile Phe Ser Gln Ile Ile Thr
     50                  55                  60

gag ttg gag aac cct tat caa ttc cag ctg gag aat gac ata cag gca    240
Glu Leu Glu Asn Pro Tyr Gln Phe Gln Leu Glu Asn Asp Ile Gln Ala
 65                  70                  75                  80

ccg agt ttt att ctt tac agt aat gaa cgc ata act att cgt ctt gtt    288
Pro Ser Phe Ile Leu Tyr Ser Asn Glu Arg Ile Thr Ile Arg Leu Val
                 85                  90                  95

atg tgg ctc cca ttg cag gga aaa tta gat cgg aca cct tat tcc tac    336
Met Trp Leu Pro Leu Gln Gly Lys Leu Asp Arg Thr Pro Tyr Ser Tyr
            100                 105                 110

gaa gaa gca cat gat cat aat ttt gac ttt tgg aca gtg aat ttt ttt    384
Glu Glu Ala His Asp His Asn Phe Asp Phe Trp Thr Val Asn Phe Phe
        115                 120                 125

gga ggt ggc tat cga act cgg ctc tat gac tat gat tac gat aaa gtt    432
Gly Gly Gly Tyr Arg Thr Arg Leu Tyr Asp Tyr Asp Tyr Asp Lys Val
    130                 135                 140

agt ggc gta aat aac gaa gtt gta gaa ctt aat tgt tat gga gat aag    480
Ser Gly Val Asn Asn Glu Val Val Glu Leu Asn Cys Tyr Gly Asp Lys
145                 150                 155                 160

att ctt tcc ccg aat aca gtt atg ttt tat ttt cgt agt aag gat gtt    528
```

Ile Leu Ser Pro Asn Thr Val Met Phe Tyr Phe Arg Ser Lys Asp Val
165 170 175

cat act caa tat ccg cct gat gaa tta tca gta tcg ctc aat tta ata 576
His Thr Gln Tyr Pro Pro Asp Glu Leu Ser Val Ser Leu Asn Leu Ile
180 185 190

gtg cga cca ata aaa tcg aag cat caa tac gaa ttt cag ata gat tca 624
Val Arg Pro Ile Lys Ser Lys His Gln Tyr Glu Phe Gln Ile Asp Ser
195 200 205

gat gca ttg gaa gga aaa ata gag gca aga att aaa aag gga aga tat 672
Asp Ala Leu Glu Gly Lys Ile Glu Ala Arg Ile Lys Lys Gly Arg Tyr
210 215 220

gag cgc tac gct ttt caa aat gtg tta tat aac ggc ctg ctg agt ctt 720
Glu Arg Tyr Ala Phe Gln Asn Val Leu Tyr Asn Gly Leu Leu Ser Leu
225 230 235 240

gaa aat gaa aaa agt cgt caa ctg gtt cac aaa gtg tct ctt tgt aac 768
Glu Asn Glu Lys Ser Arg Gln Leu Val His Lys Val Ser Leu Cys Asn
245 250 255

cat cga gaa gag ata cga tta atc gct tat gaa gct tta ctt aag cac 816
His Arg Glu Glu Ile Arg Leu Ile Ala Tyr Glu Ala Leu Leu Lys His
260 265 270

gcc caa aaa aaa ggt aat gtg agt gat ata aag agc att agt gaa caa 864
Ala Gln Lys Lys Gly Asn Val Ser Asp Ile Lys Ser Ile Ser Glu Gln
275 280 285

gca ttt aaa gac caa agc ctc tat atc aaa aat aag att tct cac agt 912
Ala Phe Lys Asp Gln Ser Leu Tyr Ile Lys Asn Lys Ile Ser His Ser
290 295 300

att gga agc atg cca tgc atg agt cca aaa ccc cgc taa 951
Ile Gly Ser Met Pro Cys Met Ser Pro Lys Pro Arg
305 310 315

<210> 18
<211> 316
<212> PRT
<213> Yersinia pestis

<400> 18
Met Leu Leu Asn Asn Ile Thr Pro Val Asn Lys Ser Leu Thr Leu Gln
1 5 10 15

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Asp Leu Leu Gly Ile Leu Ser His Ser Ser Ala Ile Ser Asn Val Ala
             20                  25                  30

Asn Gly Ile Tyr Val Glu Ser Glu Ile Leu Glu Val Gly Ser Trp Leu
         35                  40                  45

Ser Ala Tyr Ala Ala Asn Lys Asp Glu Ile Phe Ser Gln Ile Ile Thr
     50                  55                  60

Glu Leu Glu Asn Pro Tyr Gln Phe Gln Leu Glu Asn Asp Ile Gln Ala
 65                  70                  75                  80

Pro Ser Phe Ile Leu Tyr Ser Asn Glu Arg Ile Thr Ile Arg Leu Val
                 85                  90                  95

Met Trp Leu Pro Leu Gln Gly Lys Leu Asp Arg Thr Pro Tyr Ser Tyr
            100                 105                 110

Glu Glu Ala His Asp His Asn Phe Asp Phe Trp Thr Val Asn Phe Phe
        115                 120                 125

Gly Gly Gly Tyr Arg Thr Arg Leu Tyr Asp Tyr Asp Tyr Asp Lys Val
    130                 135                 140

Ser Gly Val Asn Asn Glu Val Val Glu Leu Asn Cys Tyr Gly Asp Lys
145                 150                 155                 160

Ile Leu Ser Pro Asn Thr Val Met Phe Tyr Phe Arg Ser Lys Asp Val
                165                 170                 175

His Thr Gln Tyr Pro Pro Asp Glu Leu Ser Val Ser Leu Asn Leu Ile
            180                 185                 190

Val Arg Pro Ile Lys Ser Lys His Gln Tyr Glu Phe Gln Ile Asp Ser
        195                 200                 205

Asp Ala Leu Glu Gly Lys Ile Glu Ala Arg Ile Lys Lys Gly Arg Tyr
    210                 215                 220

Glu Arg Tyr Ala Phe Gln Asn Val Leu Tyr Asn Gly Leu Leu Ser Leu
225                 230                 235                 240

Glu Asn Glu Lys Ser Arg Gln Leu Val His Lys Val Ser Leu Cys Asn
                245                 250                 255

His Arg Glu Glu Ile Arg Leu Ile Ala Tyr Glu Ala Leu Leu Lys His
            260                 265                 270
```

```
Ala Gln Lys Lys Gly Asn Val Ser Asp Ile Lys Ser Ile Ser Glu Gln
        275                 280                 285

Ala Phe Lys Asp Gln Ser Leu Tyr Ile Lys Asn Lys Ile Ser His Ser
    290                 295                 300

Ile Gly Ser Met Pro Cys Met Ser Pro Lys Pro Arg
305                 310                 315



<210> 19
<211> 1347
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(1347)

<400> 19
atg aag gtt acg gtt ttt ggt att ggt tat gtg gga ctt gtt caa gct      48
Met Lys Val Thr Val Phe Gly Ile Gly Tyr Val Gly Leu Val Gln Ala
1               5                   10                  15

aca gtg ctt gcc gag gtg ggg cat gat gtc ctt tgt atc gat att gat      96
Thr Val Leu Ala Glu Val Gly His Asp Val Leu Cys Ile Asp Ile Asp
            20                  25                  30

gct aat aaa gtt gcc gat ttg aaa aaa ggc cgt att gct att ttt gag     144
Ala Asn Lys Val Ala Asp Leu Lys Lys Gly Arg Ile Ala Ile Phe Glu
        35                  40                  45

ccg ggc ttg gct ccg ttg gtc aaa gaa aac tat gag gca ggc aga tta     192
Pro Gly Leu Ala Pro Leu Val Lys Glu Asn Tyr Glu Ala Gly Arg Leu
    50                  55                  60

cag ttt tca aca gat gcg caa gct ggt gtg gca cat ggc gtc att caa     240
Gln Phe Ser Thr Asp Ala Gln Ala Gly Val Ala His Gly Val Ile Gln
65                  70                  75                  80

ttt att gct gtg ggt aca cct cct gat gaa gac ggt gct gcc gat ctt     288
Phe Ile Ala Val Gly Thr Pro Pro Asp Glu Asp Gly Ala Ala Asp Leu
                85                  90                  95

aaa tat gtc ctt gat gtg gcc agt acc att ggc acg tat atg gac tca     336
Lys Tyr Val Leu Asp Val Ala Ser Thr Ile Gly Thr Tyr Met Asp Ser
```

```
            100                 105                 110

cct aag gtc att atc gat aaa tct aca gtg ccc gtg ggg aca gcg gat    384
Pro Lys Val Ile Ile Asp Lys Ser Thr Val Pro Val Gly Thr Ala Asp
        115                 120                 125

aaa gta cat caa gtt ata caa gct att ttg gag cag cgc ggt gag aag    432
Lys Val His Gln Val Ile Gln Ala Ile Leu Glu Gln Arg Gly Glu Lys
    130                 135                 140

ata gat ttt agt gtg gta tca aat cct gag ttt tta aaa gag ggg gcc    480
Ile Asp Phe Ser Val Val Ser Asn Pro Glu Phe Leu Lys Glu Gly Ala
145                 150                 155                 160

gca gtt gct gat tgt aaa cgg cct gaa cgt att gtt att ggt att gat    528
Ala Val Ala Asp Cys Lys Arg Pro Glu Arg Ile Val Ile Gly Ile Asp
                165                 170                 175

acg gat gac agt ggt gct cta gag tta atc agt gaa tta tac gaa cct    576
Thr Asp Asp Ser Gly Ala Leu Glu Leu Ile Ser Glu Leu Tyr Glu Pro
            180                 185                 190

ttt aat cga aat cat gat cgt atg cta gta atg gat atc cgt agt gca    624
Phe Asn Arg Asn His Asp Arg Met Leu Val Met Asp Ile Arg Ser Ala
        195                 200                 205

gaa ctg aca aag tat gct gca aac ggc atg ctg gca acg aaa ata agt    672
Glu Leu Thr Lys Tyr Ala Ala Asn Gly Met Leu Ala Thr Lys Ile Ser
    210                 215                 220

ttc atg aat gag att gct aat att gct gag cga tta ggg gct gat atc    720
Phe Met Asn Glu Ile Ala Asn Ile Ala Glu Arg Leu Gly Ala Asp Ile
225                 230                 235                 240

gaa aaa gtt cga cag ggc atc ggt tcc gat tca cgt att gga tac cat    768
Glu Lys Val Arg Gln Gly Ile Gly Ser Asp Ser Arg Ile Gly Tyr His
                245                 250                 255

ttc att tat tct ggt tgt ggt tat ggg ggg tct tgt ttc cca aaa gac    816
Phe Ile Tyr Ser Gly Cys Gly Tyr Gly Gly Ser Cys Phe Pro Lys Asp
            260                 265                 270

atc caa gca tta att cgt act gca gaa gat aag ggt tat aag ccc cag    864
Ile Gln Ala Leu Ile Arg Thr Ala Glu Asp Lys Gly Tyr Lys Pro Gln
        275                 280                 285

cta ttg cag gct gtc gag caa atc aat aat cag cag aag tat aag tta    912
Leu Leu Gln Ala Val Glu Gln Ile Asn Asn Gln Gln Lys Tyr Lys Leu
```

290 295 300

act gaa ttc att aaa agt cat ttt aat tcg cag tta gct gga aaa aca 960
Thr Glu Phe Ile Lys Ser His Phe Asn Ser Gln Leu Ala Gly Lys Thr
305 310 315 320

ttt gct gtc tgg gga ttg gcc ttt aag ccc aac acc gat gat atg cgt 1008
Phe Ala Val Trp Gly Leu Ala Phe Lys Pro Asn Thr Asp Asp Met Arg
325 330 335

gag gca ccg agc cgt gtg gta atg gaa tca ttg tgg gaa gcc ggg gct 1056
Glu Ala Pro Ser Arg Val Val Met Glu Ser Leu Trp Glu Ala Gly Ala
340 345 350

aca att caa gca tac gat ccc gaa gca atg gat gag acg caa cgc att 1104
Thr Ile Gln Ala Tyr Asp Pro Glu Ala Met Asp Glu Thr Gln Arg Ile
355 360 365

tat ggt gca aga gat gat ttg aga tta atg ggg act aaa gag tct gca 1152
Tyr Gly Ala Arg Asp Asp Leu Arg Leu Met Gly Thr Lys Glu Ser Ala
370 375 380

tta cag gga gct gat gcc ttg att att tgt act gaa tgg caa agt ttt 1200
Leu Gln Gly Ala Asp Ala Leu Ile Ile Cys Thr Glu Trp Gln Ser Phe
385 390 395 400

cgt gct cca gat ttt gat atg atc aag tca agg tta aag cac cct gtt 1248
Arg Ala Pro Asp Phe Asp Met Ile Lys Ser Arg Leu Lys His Pro Val
405 410 415

att ttt gat ggg cgt aat ttg tac gat cca gaa cgc cta aat agt cgt 1296
Ile Phe Asp Gly Arg Asn Leu Tyr Asp Pro Glu Arg Leu Asn Ser Arg
420 425 430

ggg ttc act tat tat gga att ggg cgt ggt gtt tcg att aat cta tca 1344
Gly Phe Thr Tyr Tyr Gly Ile Gly Arg Gly Val Ser Ile Asn Leu Ser
435 440 445

tag 1347

<210> 20
<211> 448
<212> PRT
<213> Yersinia pestis

<400> 20

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Met Lys Val Thr Val Phe Gly Ile Gly Tyr Val Gly Leu Val Gln Ala
1               5                   10                  15

Thr Val Leu Ala Glu Val Gly His Asp Val Leu Cys Ile Asp Ile Asp
            20                  25                  30

Ala Asn Lys Val Ala Asp Leu Lys Lys Gly Arg Ile Ala Ile Phe Glu
        35                  40                  45

Pro Gly Leu Ala Pro Leu Val Lys Glu Asn Tyr Glu Ala Gly Arg Leu
    50                  55                  60

Gln Phe Ser Thr Asp Ala Gln Ala Gly Val Ala His Gly Val Ile Gln
65                  70                  75                  80

Phe Ile Ala Val Gly Thr Pro Pro Asp Glu Asp Gly Ala Ala Asp Leu
                85                  90                  95

Lys Tyr Val Leu Asp Val Ala Ser Thr Ile Gly Thr Tyr Met Asp Ser
            100                 105                 110

Pro Lys Val Ile Ile Asp Lys Ser Thr Val Pro Val Gly Thr Ala Asp
        115                 120                 125

Lys Val His Gln Val Ile Gln Ala Ile Leu Glu Gln Arg Gly Glu Lys
    130                 135                 140

Ile Asp Phe Ser Val Val Ser Asn Pro Glu Phe Leu Lys Glu Gly Ala
145                 150                 155                 160

Ala Val Ala Asp Cys Lys Arg Pro Glu Arg Ile Val Ile Gly Ile Asp
                165                 170                 175

Thr Asp Asp Ser Gly Ala Leu Glu Leu Ile Ser Glu Leu Tyr Glu Pro
            180                 185                 190

Phe Asn Arg Asn His Asp Arg Met Leu Val Met Asp Ile Arg Ser Ala
        195                 200                 205

Glu Leu Thr Lys Tyr Ala Ala Asn Gly Met Leu Ala Thr Lys Ile Ser
    210                 215                 220

Phe Met Asn Glu Ile Ala Asn Ile Ala Glu Arg Leu Gly Ala Asp Ile
225                 230                 235                 240

Glu Lys Val Arg Gln Gly Ile Gly Ser Asp Ser Arg Ile Gly Tyr His
                245                 250                 255
```

```
Phe Ile Tyr Ser Gly Cys Gly Tyr Gly Gly Ser Cys Phe Pro Lys Asp
            260                 265                 270

Ile Gln Ala Leu Ile Arg Thr Ala Glu Asp Lys Gly Tyr Lys Pro Gln
        275                 280                 285

Leu Leu Gln Ala Val Glu Gln Ile Asn Asn Gln Gln Lys Tyr Lys Leu
    290                 295                 300

Thr Glu Phe Ile Lys Ser His Phe Asn Ser Gln Leu Ala Gly Lys Thr
305                 310                 315                 320

Phe Ala Val Trp Gly Leu Ala Phe Lys Pro Asn Thr Asp Asp Met Arg
                325                 330                 335

Glu Ala Pro Ser Arg Val Val Met Glu Ser Leu Trp Glu Ala Gly Ala
            340                 345                 350

Thr Ile Gln Ala Tyr Asp Pro Glu Ala Met Asp Glu Thr Gln Arg Ile
        355                 360                 365

Tyr Gly Ala Arg Asp Asp Leu Arg Leu Met Gly Thr Lys Glu Ser Ala
    370                 375                 380

Leu Gln Gly Ala Asp Ala Leu Ile Ile Cys Thr Glu Trp Gln Ser Phe
385                 390                 395                 400

Arg Ala Pro Asp Phe Asp Met Ile Lys Ser Arg Leu Lys His Pro Val
                405                 410                 415

Ile Phe Asp Gly Arg Asn Leu Tyr Asp Pro Glu Arg Leu Asn Ser Arg
            420                 425                 430

Gly Phe Thr Tyr Tyr Gly Ile Gly Arg Gly Val Ser Ile Asn Leu Ser
        435                 440                 445
```

<210> 21
<211> 822
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(822)

<400> 21

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atg aag aat att aag gtt tat caa tat atc aag tgg gtc att atg cca     48
Met Lys Asn Ile Lys Val Tyr Gln Tyr Ile Lys Trp Val Ile Met Pro
1               5                   10                  15

act att gtg ctg tta atg tgg caa atg ctc gcc ata tcg ggc tgg ata     96
Thr Ile Val Leu Leu Met Trp Gln Met Leu Ala Ile Ser Gly Trp Ile
            20                  25                  30

caa ccc aca ata ctt cca tca cca gta gcc gtt gtg gtg cgc tgg ttc     144
Gln Pro Thr Ile Leu Pro Ser Pro Val Ala Val Val Val Arg Trp Phe
        35                  40                  45

gat tat ttc tta ccc tat gaa gcc tat aac cca gaa aca tca aac tgg     192
Asp Tyr Phe Leu Pro Tyr Glu Ala Tyr Asn Pro Glu Thr Ser Asn Trp
    50                  55                  60

ctg atg tgg agt ctt tca ggg gag tta ctg cat gat gcc tgg gcg agt     240
Leu Met Trp Ser Leu Ser Gly Glu Leu Leu His Asp Ala Trp Ala Ser
65                  70                  75                  80

atc tac cgc gta att att ggt ttt cta atc ggt gct ctt ctt gct cta     288
Ile Tyr Arg Val Ile Ile Gly Phe Leu Ile Gly Ala Leu Leu Ala Leu
                85                  90                  95

cca tta gga tta tgg gtg ggt tcc agt aaa att ggc aat gac cta atg     336
Pro Leu Gly Leu Trp Val Gly Ser Ser Lys Ile Gly Asn Asp Leu Met
            100                 105                 110

aac cct tta att cag ttt ctt cgc ccc att ccg cca att gca tat att     384
Asn Pro Leu Ile Gln Phe Leu Arg Pro Ile Pro Pro Ile Ala Tyr Ile
        115                 120                 125

cca tta gcg atg ctg tgg ttc ggc ctg ggg aat ccg ccg gca ttt ttt     432
Pro Leu Ala Met Leu Trp Phe Gly Leu Gly Asn Pro Pro Ala Phe Phe
    130                 135                 140

ttg ata agt ata ggg gct ttt ttc cca ata ctg att aat acc atc gcg     480
Leu Ile Ser Ile Gly Ala Phe Phe Pro Ile Leu Ile Asn Thr Ile Ala
145                 150                 155                 160

ggg gtc cgt aat gtg gat ggc ata tat atc ctg gct gca cgc aat cta     528
Gly Val Arg Asn Val Asp Gly Ile Tyr Ile Leu Ala Ala Arg Asn Leu
                165                 170                 175

ggc gca ggt caa gcc acg atg ttt cgc cga att att ctt ccg gcg gcc     576
Gly Ala Gly Gln Ala Thr Met Phe Arg Arg Ile Ile Leu Pro Ala Ala
            180                 185                 190
```

```
act cct tat att ctt aca ggg atg cga gtt ggt ata ggg acc gcg ttt    624
Thr Pro Tyr Ile Leu Thr Gly Met Arg Val Gly Ile Gly Thr Ala Phe
        195                 200                 205

att tgc gtg att gtg gca gaa atg atc gcc gtt aat agc ggt gtt ggc    672
Ile Cys Val Ile Val Ala Glu Met Ile Ala Val Asn Ser Gly Val Gly
    210                 215                 220

tac cga att ctg gaa gcg cgc gaa tat atg tgg tcc gat aaa gta ata    720
Tyr Arg Ile Leu Glu Ala Arg Glu Tyr Met Trp Ser Asp Lys Val Ile
225                 230                 235                 240

gca ggc atg ttc aca att ggt ttt ctt ggc ctg gtc att gat tta tgc    768
Ala Gly Met Phe Thr Ile Gly Phe Leu Gly Leu Val Ile Asp Leu Cys
                245                 250                 255

atg gat cgc ctg aat cgg cgt ctt tta cgc tgg cac aga gga ata ggc    816
Met Asp Arg Leu Asn Arg Arg Leu Leu Arg Trp His Arg Gly Ile Gly
            260                 265                 270

aac tga                                                            822
Asn


<210> 22
<211> 273
<212> PRT
<213> Yersinia pestis

<400> 22
Met Lys Asn Ile Lys Val Tyr Gln Tyr Ile Lys Trp Val Ile Met Pro
1               5                   10                  15

Thr Ile Val Leu Leu Met Trp Gln Met Leu Ala Ile Ser Gly Trp Ile
            20                  25                  30

Gln Pro Thr Ile Leu Pro Ser Pro Val Ala Val Val Val Arg Trp Phe
        35                  40                  45

Asp Tyr Phe Leu Pro Tyr Glu Ala Tyr Asn Pro Glu Thr Ser Asn Trp
    50                  55                  60

Leu Met Trp Ser Leu Ser Gly Glu Leu Leu His Asp Ala Trp Ala Ser
65                  70                  75                  80

Ile Tyr Arg Val Ile Ile Gly Phe Leu Ile Gly Ala Leu Leu Ala Leu
                85                  90                  95
```

```
Pro Leu Gly Leu Trp Val Gly Ser Ser Lys Ile Gly Asn Asp Leu Met
            100                 105                 110

Asn Pro Leu Ile Gln Phe Leu Arg Pro Ile Pro Pro Ile Ala Tyr Ile
        115                 120                 125

Pro Leu Ala Met Leu Trp Phe Gly Leu Gly Asn Pro Pro Ala Phe Phe
    130                 135                 140

Leu Ile Ser Ile Gly Ala Phe Phe Pro Ile Leu Ile Asn Thr Ile Ala
145                 150                 155                 160

Gly Val Arg Asn Val Asp Gly Ile Tyr Ile Leu Ala Ala Arg Asn Leu
                165                 170                 175

Gly Ala Gly Gln Ala Thr Met Phe Arg Arg Ile Ile Leu Pro Ala Ala
            180                 185                 190

Thr Pro Tyr Ile Leu Thr Gly Met Arg Val Gly Ile Gly Thr Ala Phe
        195                 200                 205

Ile Cys Val Ile Val Ala Glu Met Ile Ala Val Asn Ser Gly Val Gly
    210                 215                 220

Tyr Arg Ile Leu Glu Ala Arg Glu Tyr Met Trp Ser Asp Lys Val Ile
225                 230                 235                 240

Ala Gly Met Phe Thr Ile Gly Phe Leu Gly Leu Val Ile Asp Leu Cys
                245                 250                 255

Met Asp Arg Leu Asn Arg Arg Leu Leu Arg Trp His Arg Gly Ile Gly
            260                 265                 270

Asn



<210> 23
<211> 891
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(891)

<400> 23
atg agc cac cct gtt ttt gtc cgc cct gag ctg gta gtg gat aac gtc      48
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```
Met Ser His Pro Val Phe Val Arg Pro Glu Leu Val Val Asp Asn Val
1               5                   10                  15

act gtc act tat aac aat ggt cat act gcc att tat gac gcc agc ttt      96
Thr Val Thr Tyr Asn Asn Gly His Thr Ala Ile Tyr Asp Ala Ser Phe
            20                  25                  30

tca cta acg ggt ggg acg atc tgt gca ctg gta ggt gtt aat ggc agc     144
Ser Leu Thr Gly Gly Thr Ile Cys Ala Leu Val Gly Val Asn Gly Ser
        35                  40                  45

ggt aaa tcg acc tta ttt aaa agc att atg ggg tta gtc aag ccc agt     192
Gly Lys Ser Thr Leu Phe Lys Ser Ile Met Gly Leu Val Lys Pro Ser
    50                  55                  60

gtg ggc aaa gtg gaa ctg agt cac aaa cct atc agt cat gca cta aaa     240
Val Gly Lys Val Glu Leu Ser His Lys Pro Ile Ser His Ala Leu Lys
65                  70                  75                  80

caa aat acg att gct tat gta cca cag aca gaa gat gtc gat tgg aac     288
Gln Asn Thr Ile Ala Tyr Val Pro Gln Thr Glu Asp Val Asp Trp Asn
                85                  90                  95

ttc cct gtg ctt gtg gaa gat gtc gtg atg atg ggc cgt tac ggt aaa     336
Phe Pro Val Leu Val Glu Asp Val Val Met Met Gly Arg Tyr Gly Lys
            100                 105                 110

atg aat ttt cta cga att ccc agt cgt gaa gac aaa gcc att gtg aat     384
Met Asn Phe Leu Arg Ile Pro Ser Arg Glu Asp Lys Ala Ile Val Asn
        115                 120                 125

aaa tcc att gaa cga gtt ggg tta acg gca ttg cgt tca cgg caa att     432
Lys Ser Ile Glu Arg Val Gly Leu Thr Ala Leu Arg Ser Arg Gln Ile
    130                 135                 140

ggt gaa ctg tct ggt ggc cag aaa aaa cgt gtt ttc ttg gcc cga gcc     480
Gly Glu Leu Ser Gly Gly Gln Lys Lys Arg Val Phe Leu Ala Arg Ala
145                 150                 155                 160

ctt gcc caa caa ggc aca ctc tta cta ctg gat gag cca ttt acc ggc     528
Leu Ala Gln Gln Gly Thr Leu Leu Leu Leu Asp Glu Pro Phe Thr Gly
                165                 170                 175

gtt gac gtc aaa act gaa aat gcc att att gag tta ctg caa tct cta     576
Val Asp Val Lys Thr Glu Asn Ala Ile Ile Glu Leu Leu Gln Ser Leu
            180                 185                 190

cgt gac gaa ggc cat ctg att ctg gtt tca act cat aac cta ggc agc     624
```

```
Arg Asp Glu Gly His Leu Ile Leu Val Ser Thr His Asn Leu Gly Ser
        195                 200                 205

gtg ccg gaa ttt tgt gat cac gtc atc cta att aat cag acg gtg ctg    672
Val Pro Glu Phe Cys Asp His Val Ile Leu Ile Asn Gln Thr Val Leu
    210                 215                 220

gcc gcg ggc cca att gaa acg aca ttt acc cag aaa aac ctc gag atg    720
Ala Ala Gly Pro Ile Glu Thr Thr Phe Thr Gln Lys Asn Leu Glu Met
225                 230                 235                 240

acc ttt ggc ggg gta ttg cgc cat atc aat ctg tcg ggg acg gca ctg    768
Thr Phe Gly Gly Val Leu Arg His Ile Asn Leu Ser Gly Thr Ala Leu
                245                 250                 255

cat gat gat aat gat ccg cgc acc gtc acc gta ata act gat gat gaa    816
His Asp Asp Asn Asp Pro Arg Thr Val Thr Val Ile Thr Asp Asp Glu
            260                 265                 270

cgc ccc gca gta ttt tat ggt cat act aaa aat gat ccg cct gca caa    864
Arg Pro Ala Val Phe Tyr Gly His Thr Lys Asn Asp Pro Pro Ala Gln
        275                 280                 285

agc cag tca aag gag caa aat tcc tga                                891
Ser Gln Ser Lys Glu Gln Asn Ser
    290                 295


<210> 24
<211> 296
<212> PRT
<213> Yersinia pestis

<400> 24
Met Ser His Pro Val Phe Val Arg Pro Glu Leu Val Val Asp Asn Val
1               5                   10                  15

Thr Val Thr Tyr Asn Asn Gly His Thr Ala Ile Tyr Asp Ala Ser Phe
            20                  25                  30

Ser Leu Thr Gly Gly Thr Ile Cys Ala Leu Val Gly Val Asn Gly Ser
        35                  40                  45

Gly Lys Ser Thr Leu Phe Lys Ser Ile Met Gly Leu Val Lys Pro Ser
    50                  55                  60

Val Gly Lys Val Glu Leu Ser His Lys Pro Ile Ser His Ala Leu Lys
65                  70                  75                  80
```

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Gln Asn Thr Ile Ala Tyr Val Pro Gln Thr Glu Asp Val Asp Trp Asn
                85                  90                  95

Phe Pro Val Leu Val Glu Asp Val Val Met Met Gly Arg Tyr Gly Lys
            100                 105                 110

Met Asn Phe Leu Arg Ile Pro Ser Arg Glu Asp Lys Ala Ile Val Asn
        115                 120                 125

Lys Ser Ile Glu Arg Val Gly Leu Thr Ala Leu Arg Ser Arg Gln Ile
    130                 135                 140

Gly Glu Leu Ser Gly Gly Gln Lys Lys Arg Val Phe Leu Ala Arg Ala
145                 150                 155                 160

Leu Ala Gln Gln Gly Thr Leu Leu Leu Leu Asp Glu Pro Phe Thr Gly
                165                 170                 175

Val Asp Val Lys Thr Glu Asn Ala Ile Ile Glu Leu Leu Gln Ser Leu
            180                 185                 190

Arg Asp Glu Gly His Leu Ile Leu Val Ser Thr His Asn Leu Gly Ser
        195                 200                 205

Val Pro Glu Phe Cys Asp His Val Ile Leu Ile Asn Gln Thr Val Leu
    210                 215                 220

Ala Ala Gly Pro Ile Glu Thr Thr Phe Thr Gln Lys Asn Leu Glu Met
225                 230                 235                 240

Thr Phe Gly Gly Val Leu Arg His Ile Asn Leu Ser Gly Thr Ala Leu
                245                 250                 255

His Asp Asp Asn Asp Pro Arg Thr Val Thr Val Ile Thr Asp Asp Glu
            260                 265                 270

Arg Pro Ala Val Phe Tyr Gly His Thr Lys Asn Asp Pro Pro Ala Gln
        275                 280                 285

Ser Gln Ser Lys Glu Gln Asn Ser
    290                 295


<210> 25
<211> 213
<212> DNA
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<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(213)

<400> 25
atg agt ttc aag tca ata aat aaa aac gca gat ttg tac gtg act tgc     48
Met Ser Phe Lys Ser Ile Asn Lys Asn Ala Asp Leu Tyr Val Thr Cys
 1               5                  10                  15

agt ggc ctc gaa gag gcg ggg tcc atg gac ggg ccg agt cac gaa ggc     96
Ser Gly Leu Glu Glu Ala Gly Ser Met Asp Gly Pro Ser His Glu Gly
            20                  25                  30

aac cag cac aca ggc agc ttg aag cct gat ggg tat att atc att caa    144
Asn Gln His Thr Gly Ser Leu Lys Pro Asp Gly Tyr Ile Ile Ile Gln
        35                  40                  45

gaa aat gat tta att tct gga ttt gat aac aca gtc ggc ata gct aat    192
Glu Asn Asp Leu Ile Ser Gly Phe Asp Asn Thr Val Gly Ile Ala Asn
    50                  55                  60

aac cgt ttc agg aga tgt taa                                        213
Asn Arg Phe Arg Arg Cys
65                  70


<210> 26
<211> 70
<212> PRT
<213> Yersinia pestis

<400> 26
Met Ser Phe Lys Ser Ile Asn Lys Asn Ala Asp Leu Tyr Val Thr Cys
 1               5                  10                  15

Ser Gly Leu Glu Glu Ala Gly Ser Met Asp Gly Pro Ser His Glu Gly
            20                  25                  30

Asn Gln His Thr Gly Ser Leu Lys Pro Asp Gly Tyr Ile Ile Ile Gln
        35                  40                  45

Glu Asn Asp Leu Ile Ser Gly Phe Asp Asn Thr Val Gly Ile Ala Asn
    50                  55                  60

Asn Arg Phe Arg Arg Cys
65                  70
```

<210> 27
<211> 657
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(657)

<400> 27
atg cag aaa gaa aag ctt tcc gct ttg atg gat gga gaa act ctc gat 48
Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Thr Leu Asp
1 5 10 15

agc gag ctg ctg ggg att tta tcg aaa gat aag gcg tta cag caa agc 96
Ser Glu Leu Leu Gly Ile Leu Ser Lys Asp Lys Ala Leu Gln Gln Ser
20 25 30

tgg cag agc tac cat tta atc cgt gac act cta cgc gga gac gtt ggc 144
Trp Gln Ser Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
35 40 45

aat gtt tta cat ctg gat att gct agt cgt gta gca gaa gcg ctc aag 192
Asn Val Leu His Leu Asp Ile Ala Ser Arg Val Ala Glu Ala Leu Lys
50 55 60

aac gag cca gcg cgc ttg att cct att gct ata cct gaa tct cag cca 240
Asn Glu Pro Ala Arg Leu Ile Pro Ile Ala Ile Pro Glu Ser Gln Pro
65 70 75 80

cag cca cat ctt tgg cag aaa atg cct ttc tgg caa aaa gtc cgt cca 288
Gln Pro His Leu Trp Gln Lys Met Pro Phe Trp Gln Lys Val Arg Pro
85 90 95

tgg gcc agt cag att act cag gtg gga atg gcc gct tgt gtt tct ctc 336
Trp Ala Ser Gln Ile Thr Gln Val Gly Met Ala Ala Cys Val Ser Leu
100 105 110

gct gtc att gtt ggt gtt caa caa tat aac caa ccg gca caa aat tat 384
Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ala Gln Asn Tyr
115 120 125

tta caa cct gaa tca ccg gcg ttt aat acc ttg cca atg atg ggt aaa 432
Leu Gln Pro Glu Ser Pro Ala Phe Asn Thr Leu Pro Met Met Gly Lys
130 135 140

```
gca tca cca gtc agt ttt ggt gtc cct gct gat ggt tct ttt ggt act      480
Ala Ser Pro Val Ser Phe Gly Val Pro Ala Asp Gly Ser Phe Gly Thr
145                 150                 155                 160

aat caa cag aat cag gtt caa gag cag cgt cgg cgc gtc aac atg atg      528
Asn Gln Gln Asn Gln Val Gln Glu Gln Arg Arg Arg Val Asn Met Met
                165                 170                 175

act caa ttg caa gat ttt gaa ttg caa cgt cgt ttg cca caa act gat      576
Thr Gln Leu Gln Asp Phe Glu Leu Gln Arg Arg Leu Pro Gln Thr Asp
            180                 185                 190

gta ttg cag cag cct tca gat tca acg caa gcc gca att caa gtc cct      624
Val Leu Gln Gln Pro Ser Asp Ser Thr Gln Ala Ala Ile Gln Val Pro
        195                 200                 205

gga act caa tcc tta gga atg cag cag cag taa                          657
Gly Thr Gln Ser Leu Gly Met Gln Gln Gln
    210                 215


<210> 28
<211> 218
<212> PRT
<213> Yersinia pestis

<400> 28
Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Thr Leu Asp
1               5                   10                  15

Ser Glu Leu Leu Gly Ile Leu Ser Lys Asp Lys Ala Leu Gln Gln Ser
            20                  25                  30

Trp Gln Ser Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
        35                  40                  45

Asn Val Leu His Leu Asp Ile Ala Ser Arg Val Ala Glu Ala Leu Lys
    50                  55                  60

Asn Glu Pro Ala Arg Leu Ile Pro Ile Ala Ile Pro Glu Ser Gln Pro
65                  70                  75                  80

Gln Pro His Leu Trp Gln Lys Met Pro Phe Trp Gln Lys Val Arg Pro
                85                  90                  95

Trp Ala Ser Gln Ile Thr Gln Val Gly Met Ala Ala Cys Val Ser Leu
            100                 105                 110
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Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ala Gln Asn Tyr
115 120 125

Leu Gln Pro Glu Ser Pro Ala Phe Asn Thr Leu Pro Met Met Gly Lys
130 135 140

Ala Ser Pro Val Ser Phe Gly Val Pro Ala Asp Gly Ser Phe Gly Thr
145 150 155 160

Asn Gln Gln Asn Gln Val Gln Glu Gln Arg Arg Arg Val Asn Met Met
165 170 175

Thr Gln Leu Gln Asp Phe Glu Leu Gln Arg Arg Leu Pro Gln Thr Asp
180 185 190

Val Leu Gln Gln Pro Ser Asp Ser Thr Gln Ala Ala Ile Gln Val Pro
195 200 205

Gly Thr Gln Ser Leu Gly Met Gln Gln Gln
210 215

<210> 29
<211> 1413
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(1413)

<400> 29
ttg ctc atg cta tta cct gta att atg gct gga ggt gct ggt agc cgt 48
Leu Leu Met Leu Leu Pro Val Ile Met Ala Gly Gly Ala Gly Ser Arg
1 5 10 15

ttg tgg cca tta tcc cga gct ctt tat cct aaa caa ttt cta gcg cta 96
Leu Trp Pro Leu Ser Arg Ala Leu Tyr Pro Lys Gln Phe Leu Ala Leu
20 25 30

acg tca gat ttg acg atg cta caa gaa acc cta ttg cgt ctg gac ggc 144
Thr Ser Asp Leu Thr Met Leu Gln Glu Thr Leu Leu Arg Leu Asp Gly
35 40 45

ctt ccc cac ctt gca cca tta gtg att tgt aac gaa gaa cat cgc ttt 192
Leu Pro His Leu Ala Pro Leu Val Ile Cys Asn Glu Glu His Arg Phe

50 55 60

att atc gca gaa cag tta cgt cag aaa aat ctg gtg cat agc gga ata 240
Ile Ile Ala Glu Gln Leu Arg Gln Lys Asn Leu Val His Ser Gly Ile
65 70 75 80

gtc ttg gaa cct gtt ggg cgc aat acc gcg cca gct ata gca ttg gct 288
Val Leu Glu Pro Val Gly Arg Asn Thr Ala Pro Ala Ile Ala Leu Ala
85 90 95

gcc tta cga gca aca atg agt ggg gat gat cct cta tta ttg gta tta 336
Ala Leu Arg Ala Thr Met Ser Gly Asp Asp Pro Leu Leu Leu Val Leu
100 105 110

gca gcc gat cac gtg att cag gat aaa ctt gca ttt att cgt gcc gtc 384
Ala Ala Asp His Val Ile Gln Asp Lys Leu Ala Phe Ile Arg Ala Val
115 120 125

caa cgt gct gaa ccg ctt gct gaa gcg gga aaa ttg gtt act ttt gga 432
Gln Arg Ala Glu Pro Leu Ala Glu Ala Gly Lys Leu Val Thr Phe Gly
130 135 140

atc gtg cca aag agt ccg gaa aca gga tat gga tat att cgc caa ggg 480
Ile Val Pro Lys Ser Pro Glu Thr Gly Tyr Gly Tyr Ile Arg Gln Gly
145 150 155 160

aag caa gtc gta gat ggc gct tat cag gtt gct gct ttt gtt gag aag 528
Lys Gln Val Val Asp Gly Ala Tyr Gln Val Ala Ala Phe Val Glu Lys
165 170 175

cca gat ctg att act gca gag cgg tat ttg gct tcg ggt gac tat tat 576
Pro Asp Leu Ile Thr Ala Glu Arg Tyr Leu Ala Ser Gly Asp Tyr Tyr
180 185 190

tgg aat agc ggt atg ttt gta ttt aaa gca tct cgc tat cta cag gaa 624
Trp Asn Ser Gly Met Phe Val Phe Lys Ala Ser Arg Tyr Leu Gln Glu
195 200 205

tta gat cta cat cgt ccg gat att ttg gct gcc tgc aag caa gcc att 672
Leu Asp Leu His Arg Pro Asp Ile Leu Ala Ala Cys Lys Gln Ala Ile
210 215 220

gct ggt caa cat act gat tta gat ttt att cgt ctc aat gaa gaa gct 720
Ala Gly Gln His Thr Asp Leu Asp Phe Ile Arg Leu Asn Glu Glu Ala
225 230 235 240

ttc tct agt tgc cct gat gaa tct atc gac tat gct gtg atg gaa aaa 768
Phe Ser Ser Cys Pro Asp Glu Ser Ile Asp Tyr Ala Val Met Glu Lys

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                245                 250                 255

act agc gat gcc gtt gta gtg cca ctg gat gca cag tgg aat gat gtt      816
Thr Ser Asp Ala Val Val Val Pro Leu Asp Ala Gln Trp Asn Asp Val
            260                 265                 270

ggg tgc tgg tca gcg ctt tgg gaa att aat act aaa gat gac cat ggt      864
Gly Cys Trp Ser Ala Leu Trp Glu Ile Asn Thr Lys Asp Asp His Gly
        275                 280                 285

aat gtt att cgt ggt gat gta tta ata gaa gat act aat aat agc tac      912
Asn Val Ile Arg Gly Asp Val Leu Ile Glu Asp Thr Asn Asn Ser Tyr
    290                 295                 300

gtt tat tct caa aat agg ctc att gca act gta ggc att aat gat ttg      960
Val Tyr Ser Gln Asn Arg Leu Ile Ala Thr Val Gly Ile Asn Asp Leu
305                 310                 315                 320

gtt att gtt gaa act aaa gat gcc att tta gtt gct cat aaa gat aaa      1008
Val Ile Val Glu Thr Lys Asp Ala Ile Leu Val Ala His Lys Asp Lys
                325                 330                 335

gta caa aat gtt aaa ggg atc gtt gga cag ctt aag ctt gaa tct cga      1056
Val Gln Asn Val Lys Gly Ile Val Gly Gln Leu Lys Leu Glu Ser Arg
            340                 345                 350

tgt gaa tat cta cag cac cgg gaa gtc tat cgc cct tgg ggt tcg cat      1104
Cys Glu Tyr Leu Gln His Arg Glu Val Tyr Arg Pro Trp Gly Ser His
        355                 360                 365

gat gct att gct gaa ggt gtt cgc tac cat gtc caa cat gta acg gtg      1152
Asp Ala Ile Ala Glu Gly Val Arg Tyr His Val Gln His Val Thr Val
    370                 375                 380

aaa cca ggt caa cgt att gct act caa att cat tat cac aga gcg gaa      1200
Lys Pro Gly Gln Arg Ile Ala Thr Gln Ile His Tyr His Arg Ala Glu
385                 390                 395                 400

cat tgg att gtg gtt tct ggc att gcc aaa gta cat tat gga aaa gaa      1248
His Trp Ile Val Val Ser Gly Ile Ala Lys Val His Tyr Gly Lys Glu
                405                 410                 415

act tat ttg gtt aat gag aat gaa tcc act tat att ccc gtc ggc att      1296
Thr Tyr Leu Val Asn Glu Asn Glu Ser Thr Tyr Ile Pro Val Gly Ile
            420                 425                 430

gct cat tct att gaa aat cca ggt cag atc cct ctg gaa ata ata gag      1344
Ala His Ser Ile Glu Asn Pro Gly Gln Ile Pro Leu Glu Ile Ile Glu
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        435                 440                 445

gtt cat act ggt aat tac att tca gaa gat gat gtg gaa cga atc gat   1392
Val His Thr Gly Asn Tyr Ile Ser Glu Asp Asp Val Glu Arg Ile Asp
    450                 455                 460

gat tta ggt gta ggg tat taa                                       1413
Asp Leu Gly Val Gly Tyr
465                 470


<210> 30
<211> 470
<212> PRT
<213> Yersinia pestis

<400> 30
Leu Leu Met Leu Leu Pro Val Ile Met Ala Gly Gly Ala Gly Ser Arg
 1               5                   10                  15

Leu Trp Pro Leu Ser Arg Ala Leu Tyr Pro Lys Gln Phe Leu Ala Leu
             20                  25                  30

Thr Ser Asp Leu Thr Met Leu Gln Glu Thr Leu Leu Arg Leu Asp Gly
         35                  40                  45

Leu Pro His Leu Ala Pro Leu Val Ile Cys Asn Glu Glu His Arg Phe
     50                  55                  60

Ile Ile Ala Glu Gln Leu Arg Gln Lys Asn Leu Val His Ser Gly Ile
 65                  70                  75                  80

Val Leu Glu Pro Val Gly Arg Asn Thr Ala Pro Ala Ile Ala Leu Ala
                 85                  90                  95

Ala Leu Arg Ala Thr Met Ser Gly Asp Asp Pro Leu Leu Leu Val Leu
            100                 105                 110

Ala Ala Asp His Val Ile Gln Asp Lys Leu Ala Phe Ile Arg Ala Val
        115                 120                 125

Gln Arg Ala Glu Pro Leu Ala Glu Ala Gly Lys Leu Val Thr Phe Gly
    130                 135                 140

Ile Val Pro Lys Ser Pro Glu Thr Gly Tyr Gly Tyr Ile Arg Gln Gly
145                 150                 155                 160

Lys Gln Val Val Asp Gly Ala Tyr Gln Val Ala Ala Phe Val Glu Lys
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                165                 170                 175

Pro Asp Leu Ile Thr Ala Glu Arg Tyr Leu Ala Ser Gly Asp Tyr Tyr
            180                 185                 190

Trp Asn Ser Gly Met Phe Val Phe Lys Ala Ser Arg Tyr Leu Gln Glu
        195                 200                 205

Leu Asp Leu His Arg Pro Asp Ile Leu Ala Ala Cys Lys Gln Ala Ile
    210                 215                 220

Ala Gly Gln His Thr Asp Leu Asp Phe Ile Arg Leu Asn Glu Glu Ala
225                 230                 235                 240

Phe Ser Ser Cys Pro Asp Glu Ser Ile Asp Tyr Ala Val Met Glu Lys
                245                 250                 255

Thr Ser Asp Ala Val Val Val Pro Leu Asp Ala Gln Trp Asn Asp Val
            260                 265                 270

Gly Cys Trp Ser Ala Leu Trp Glu Ile Asn Thr Lys Asp Asp His Gly
        275                 280                 285

Asn Val Ile Arg Gly Asp Val Leu Ile Glu Asp Thr Asn Asn Ser Tyr
    290                 295                 300

Val Tyr Ser Gln Asn Arg Leu Ile Ala Thr Val Gly Ile Asn Asp Leu
305                 310                 315                 320

Val Ile Val Glu Thr Lys Asp Ala Ile Leu Val Ala His Lys Asp Lys
                325                 330                 335

Val Gln Asn Val Lys Gly Ile Val Gly Gln Leu Lys Leu Glu Ser Arg
            340                 345                 350

Cys Glu Tyr Leu Gln His Arg Glu Val Tyr Arg Pro Trp Gly Ser His
        355                 360                 365

Asp Ala Ile Ala Glu Gly Val Arg Tyr His Val Gln His Val Thr Val
    370                 375                 380

Lys Pro Gly Gln Arg Ile Ala Thr Gln Ile His Tyr His Arg Ala Glu
385                 390                 395                 400

His Trp Ile Val Val Ser Gly Ile Ala Lys Val His Tyr Gly Lys Glu
                405                 410                 415

Thr Tyr Leu Val Asn Glu Asn Glu Ser Thr Tyr Ile Pro Val Gly Ile
```

420 425 430

Ala His Ser Ile Glu Asn Pro Gly Gln Ile Pro Leu Glu Ile Ile Glu
435 440 445

Val His Thr Gly Asn Tyr Ile Ser Glu Asp Asp Val Glu Arg Ile Asp
450 455 460

Asp Leu Gly Val Gly Tyr
465 470

<210> 31
<211> 1014
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(1014)

<400> 31
atg aaa att att tat gat gga ata att aat tca ttg caa aat atg gga 48
Met Lys Ile Ile Tyr Asp Gly Ile Ile Asn Ser Leu Gln Asn Met Gly
1 5 10 15

ggg gta act gtc tat ttc tcg gag tta gtg agt cga ctt cct gca aca 96
Gly Val Thr Val Tyr Phe Ser Glu Leu Val Ser Arg Leu Pro Ala Thr
20 25 30

gat ttt tat tgg tac tca tac gca gat gaa ata tct ggt ttc ggt gtt 144
Asp Phe Tyr Trp Tyr Ser Tyr Ala Asp Glu Ile Ser Gly Phe Gly Val
35 40 45

ggt aat gtt aaa ata aaa tct aga ctt tta gag cga tat agg aat ttc 192
Gly Asn Val Lys Ile Lys Ser Arg Leu Leu Glu Arg Tyr Arg Asn Phe
50 55 60

tca tta gat act att aat tat aat tct ctt tct gta ttt cat tca tca 240
Ser Leu Asp Thr Ile Asn Tyr Asn Ser Leu Ser Val Phe His Ser Ser
65 70 75 80

tat tac cga tta cca gat ttt gac att ccg ata gtt aca aca gtt cat 288
Tyr Tyr Arg Leu Pro Asp Phe Asp Ile Pro Ile Val Thr Thr Val His
85 90 95

gat ttc aca tat gaa aag ttt gtt aat ggc cct gca aaa tgg gtg cat 336

```
Asp Phe Thr Tyr Glu Lys Phe Val Asn Gly Pro Ala Lys Trp Val His
            100                 105                 110

tcc tgg cag aaa aac cgt gcg gtt aac aat agt gat tta att att tgt    384
Ser Trp Gln Lys Asn Arg Ala Val Asn Asn Ser Asp Leu Ile Ile Cys
        115                 120                 125

gtt tcg gaa aat aca gct aaa gat ttg caa atg tat tgc tca gtt cct    432
Val Ser Glu Asn Thr Ala Lys Asp Leu Gln Met Tyr Cys Ser Val Pro
    130                 135                 140

agc aat aaa atc aga gtg ata tat aac ggt gtg tca gat aaa tat cat    480
Ser Asn Lys Ile Arg Val Ile Tyr Asn Gly Val Ser Asp Lys Tyr His
145                 150                 155                 160

tat att aag ggt gtt aaa ata acc aca aat aaa gtt att ttt gtt ggt    528
Tyr Ile Lys Gly Val Lys Ile Thr Thr Asn Lys Val Ile Phe Val Gly
                165                 170                 175

gca cgt ggt ggt tat aag aat ttt gac att gca gtg aaa gca ata tca    576
Ala Arg Gly Gly Tyr Lys Asn Phe Asp Ile Ala Val Lys Ala Ile Ser
            180                 185                 190

aaa aca cct cac ctc gaa tta tca gtt gta ggt gga ggg gca ttc act    624
Lys Thr Pro His Leu Glu Leu Ser Val Val Gly Gly Gly Ala Phe Thr
        195                 200                 205

agt aaa gaa ctg tca cta ctg aat cac tat tta cct ggt cgc tac cat    672
Ser Lys Glu Leu Ser Leu Leu Asn His Tyr Leu Pro Gly Arg Tyr His
    210                 215                 220

gga tta ggt cgc ctt agt gat gag gct ttg aat gag gca tat aat tca    720
Gly Leu Gly Arg Leu Ser Asp Glu Ala Leu Asn Glu Ala Tyr Asn Ser
225                 230                 235                 240

gct tat gcg ctg ctt tac cca tct agc tat gag ggt ttt ggt att cca    768
Ala Tyr Ala Leu Leu Tyr Pro Ser Ser Tyr Glu Gly Phe Gly Ile Pro
                245                 250                 255

ata tta gaa gcg atg agt gca gga tgt ccc gta ata tct gtt aat gta    816
Ile Leu Glu Ala Met Ser Ala Gly Cys Pro Val Ile Ser Val Asn Val
            260                 265                 270

tct tct ata cct gag gtc gca ggt gat gcc gct ata tta gtg caa aaa    864
Ser Ser Ile Pro Glu Val Ala Gly Asp Ala Ala Ile Leu Val Gln Lys
        275                 280                 285

ccg act att gat gaa cta gtt gac ggc ttg ctt gcc gta gaa agt gaa    912
```

Pro Thr Ile Asp Glu Leu Val Asp Gly Leu Leu Ala Val Glu Ser Glu
290 295 300

agg tct aaa ctt att ggc tat ggc atg aag caa gcg gct aaa ttc tca 960
Arg Ser Lys Leu Ile Gly Tyr Gly Met Lys Gln Ala Ala Lys Phe Ser
305 310 315 320

tgg gat aag tgt tat caa gaa acc tta gat gtt tat aaa gaa ttg aac 1008
Trp Asp Lys Cys Tyr Gln Glu Thr Leu Asp Val Tyr Lys Glu Leu Asn
325 330 335

aaa taa 1014
Lys

<210> 32
<211> 337
<212> PRT
<213> Yersinia pestis

<400> 32
Met Lys Ile Ile Tyr Asp Gly Ile Ile Asn Ser Leu Gln Asn Met Gly
1 5 10 15

Gly Val Thr Val Tyr Phe Ser Glu Leu Val Ser Arg Leu Pro Ala Thr
20 25 30

Asp Phe Tyr Trp Tyr Ser Tyr Ala Asp Glu Ile Ser Gly Phe Gly Val
35 40 45

Gly Asn Val Lys Ile Lys Ser Arg Leu Leu Glu Arg Tyr Arg Asn Phe
50 55 60

Ser Leu Asp Thr Ile Asn Tyr Asn Ser Leu Ser Val Phe His Ser Ser
65 70 75 80

Tyr Tyr Arg Leu Pro Asp Phe Asp Ile Pro Ile Val Thr Thr Val His
85 90 95

Asp Phe Thr Tyr Glu Lys Phe Val Asn Gly Pro Ala Lys Trp Val His
100 105 110

Ser Trp Gln Lys Asn Arg Ala Val Asn Asn Ser Asp Leu Ile Ile Cys
115 120 125

Val Ser Glu Asn Thr Ala Lys Asp Leu Gln Met Tyr Cys Ser Val Pro
130 135 140

```
Ser Asn Lys Ile Arg Val Ile Tyr Asn Gly Val Ser Asp Lys Tyr His
145                 150                 155                 160

Tyr Ile Lys Gly Val Lys Ile Thr Thr Asn Lys Val Ile Phe Val Gly
                165                 170                 175

Ala Arg Gly Gly Tyr Lys Asn Phe Asp Ile Ala Val Lys Ala Ile Ser
            180                 185                 190

Lys Thr Pro His Leu Glu Leu Ser Val Val Gly Gly Gly Ala Phe Thr
        195                 200                 205

Ser Lys Glu Leu Ser Leu Leu Asn His Tyr Leu Pro Gly Arg Tyr His
    210                 215                 220

Gly Leu Gly Arg Leu Ser Asp Glu Ala Leu Asn Glu Ala Tyr Asn Ser
225                 230                 235                 240

Ala Tyr Ala Leu Leu Tyr Pro Ser Ser Tyr Glu Gly Phe Gly Ile Pro
                245                 250                 255

Ile Leu Glu Ala Met Ser Ala Gly Cys Pro Val Ile Ser Val Asn Val
            260                 265                 270

Ser Ser Ile Pro Glu Val Ala Gly Asp Ala Ala Ile Leu Val Gln Lys
        275                 280                 285

Pro Thr Ile Asp Glu Leu Val Asp Gly Leu Leu Ala Val Glu Ser Glu
    290                 295                 300

Arg Ser Lys Leu Ile Gly Tyr Gly Met Lys Gln Ala Ala Lys Phe Ser
305                 310                 315                 320

Trp Asp Lys Cys Tyr Gln Glu Thr Leu Asp Val Tyr Lys Glu Leu Asn
                325                 330                 335

Lys
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<210> 33
<211> 990
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(990)

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<400> 33
atg tca tta aat gtt aag ctg cat cca tca ggt att att ttt act tcc    48
Met Ser Leu Asn Val Lys Leu His Pro Ser Gly Ile Ile Phe Thr Ser
1               5                   10                  15

gat gga aca tct aca ata tta gat gcg gct ctg gat agt aat ata cat    96
Asp Gly Thr Ser Thr Ile Leu Asp Ala Ala Leu Asp Ser Asn Ile His
            20                  25                  30

att gaa tac agc tgc aaa gat gga acc tgt ggt tct tgt aag gca ata    144
Ile Glu Tyr Ser Cys Lys Asp Gly Thr Cys Gly Ser Cys Lys Ala Ile
        35                  40                  45

ttg att tct ggt gaa gta gac agt gcg gaa aat acc ttt tta act gag    192
Leu Ile Ser Gly Glu Val Asp Ser Ala Glu Asn Thr Phe Leu Thr Glu
    50                  55                  60

gaa gat gtt gct aaa ggt gca atc ctc act tgt tgc tct aag gct aaa    240
Glu Asp Val Ala Lys Gly Ala Ile Leu Thr Cys Cys Ser Lys Ala Lys
65                  70                  75                  80

tct gat att gag tta gat gtt aat tat tat cca gag tta agt cat ata    288
Ser Asp Ile Glu Leu Asp Val Asn Tyr Tyr Pro Glu Leu Ser His Ile
                85                  90                  95

caa aaa aaa act tat cca tgt aaa tta gat agc att gaa ttt att ggt    336
Gln Lys Lys Thr Tyr Pro Cys Lys Leu Asp Ser Ile Glu Phe Ile Gly
            100                 105                 110

gaa gat att gcc att ctc tcc tta cgt ttg cca cca acg gcc aaa ata    384
Glu Asp Ile Ala Ile Leu Ser Leu Arg Leu Pro Pro Thr Ala Lys Ile
        115                 120                 125

cag tat ctg gcg ggc caa tac att gat tta att att aat gga cag cgc    432
Gln Tyr Leu Ala Gly Gln Tyr Ile Asp Leu Ile Ile Asn Gly Gln Arg
    130                 135                 140

cgt agt tac tct att gct aat gct cca ggt ggt aat ggc aat atc gaa    480
Arg Ser Tyr Ser Ile Ala Asn Ala Pro Gly Gly Asn Gly Asn Ile Glu
145                 150                 155                 160

tta cac gta cgt aaa gtt gtt aat ggt gta ttc agc aac atc att ttt    528
Leu His Val Arg Lys Val Val Asn Gly Val Phe Ser Asn Ile Ile Phe
                165                 170                 175

aat gag tta aaa tta cag caa ctt tta cga att gaa ggt cct caa ggg    576
Asn Glu Leu Lys Leu Gln Gln Leu Leu Arg Ile Glu Gly Pro Gln Gly
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            180                 185                 190

acc ttt ttc gtt cgt gaa gat aat ctc cct att gtt ttt ctt gct ggt    624
Thr Phe Phe Val Arg Glu Asp Asn Leu Pro Ile Val Phe Leu Ala Gly
        195                 200                 205

gga aca ggt ttt gca cca gtg aaa tca atg gtt gag gcg ttg atc aat    672
Gly Thr Gly Phe Ala Pro Val Lys Ser Met Val Glu Ala Leu Ile Asn
    210                 215                 220

aaa aat gac caa cgg cag gtt cat atc tat tgg gga atg cca gca ggg    720
Lys Asn Asp Gln Arg Gln Val His Ile Tyr Trp Gly Met Pro Ala Gly
225                 230                 235                 240

cat aat ttc tat tct gac att gcc aat gag tgg gct ata aaa cac cct    768
His Asn Phe Tyr Ser Asp Ile Ala Asn Glu Trp Ala Ile Lys His Pro
                245                 250                 255

aac att cat tat gtg cct gtt gta tca ggc gat gat agt act tgg acc    816
Asn Ile His Tyr Val Pro Val Val Ser Gly Asp Asp Ser Thr Trp Thr
            260                 265                 270

gga gcc act ggt ttt gta cat caa gcg gtg ctt gaa gat ata ccc gat    864
Gly Ala Thr Gly Phe Val His Gln Ala Val Leu Glu Asp Ile Pro Asp
        275                 280                 285

ctc agc tta ttt aat gtt tat gcc tgt ggt tca tta gcg atg att act    912
Leu Ser Leu Phe Asn Val Tyr Ala Cys Gly Ser Leu Ala Met Ile Thr
    290                 295                 300

gct gct cgt aat gat ttc atc aat cat gga tta gct gaa aat aaa ttt    960
Ala Ala Arg Asn Asp Phe Ile Asn His Gly Leu Ala Glu Asn Lys Phe
305                 310                 315                 320

ttc tct gat gcc ttt gtg cca tca aaa taa                            990
Phe Ser Asp Ala Phe Val Pro Ser Lys
                325                 330


<210> 34
<211> 329
<212> PRT
<213> Yersinia pestis

<400> 34
Met Ser Leu Asn Val Lys Leu His Pro Ser Gly Ile Ile Phe Thr Ser
 1               5                  10                  15
```

```
Asp Gly Thr Ser Thr Ile Leu Asp Ala Ala Leu Asp Ser Asn Ile His
             20                  25                  30

Ile Glu Tyr Ser Cys Lys Asp Gly Thr Cys Gly Ser Cys Lys Ala Ile
         35                  40                  45

Leu Ile Ser Gly Glu Val Asp Ser Ala Glu Asn Thr Phe Leu Thr Glu
     50                  55                  60

Glu Asp Val Ala Lys Gly Ala Ile Leu Thr Cys Cys Ser Lys Ala Lys
 65                  70                  75                  80

Ser Asp Ile Glu Leu Asp Val Asn Tyr Tyr Pro Glu Leu Ser His Ile
                 85                  90                  95

Gln Lys Lys Thr Tyr Pro Cys Lys Leu Asp Ser Ile Glu Phe Ile Gly
            100                 105                 110

Glu Asp Ile Ala Ile Leu Ser Leu Arg Leu Pro Pro Thr Ala Lys Ile
        115                 120                 125

Gln Tyr Leu Ala Gly Gln Tyr Ile Asp Leu Ile Ile Asn Gly Gln Arg
    130                 135                 140

Arg Ser Tyr Ser Ile Ala Asn Ala Pro Gly Gly Asn Gly Asn Ile Glu
145                 150                 155                 160

Leu His Val Arg Lys Val Val Asn Gly Val Phe Ser Asn Ile Ile Phe
                165                 170                 175

Asn Glu Leu Lys Leu Gln Gln Leu Leu Arg Ile Glu Gly Pro Gln Gly
            180                 185                 190

Thr Phe Phe Val Arg Glu Asp Asn Leu Pro Ile Val Phe Leu Ala Gly
        195                 200                 205

Gly Thr Gly Phe Ala Pro Val Lys Ser Met Val Glu Ala Leu Ile Asn
    210                 215                 220

Lys Asn Asp Gln Arg Gln Val His Ile Tyr Trp Gly Met Pro Ala Gly
225                 230                 235                 240

His Asn Phe Tyr Ser Asp Ile Ala Asn Glu Trp Ala Ile Lys His Pro
                245                 250                 255

Asn Ile His Tyr Val Pro Val Val Ser Gly Asp Asp Ser Thr Trp Thr
            260                 265                 270
```

```
Gly Ala Thr Gly Phe Val His Gln Ala Val Leu Glu Asp Ile Pro Asp
        275                 280                 285

Leu Ser Leu Phe Asn Val Tyr Ala Cys Gly Ser Leu Ala Met Ile Thr
    290                 295                 300

Ala Ala Arg Asn Asp Phe Ile Asn His Gly Leu Ala Glu Asn Lys Phe
305                 310                 315                 320

Phe Ser Asp Ala Phe Val Pro Ser Lys
                325
```

<210> 35
<211> 3583
<212> DNA
<213> Yersinia pestis

<400> 35

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gtgagattgt ttgcacaatt aggttggtat tttcgccgtg aatggcaccg ttatgtaggg 60
gcggtgctac tactgattat tatcgctatt ctgcaattaa ttccgcccaa gttggtgggc 120
gttatagtgg atgatatcag tacaaaacag atgtccacca atatgttatt ggtttggatt 180
ggcgtgatgc tcgcgactgc cgtggtggtc tatttgttgc gttatgtctg gcgagtctta 240
ttattcggtg cctcttatca gttggcggtg gagttgagat ctgattttta tcgtcagctg 300
agtcggcaaa ctcccggttt ttattcacgt catcgcactg gcgatttaat ggctcgcgcc 360
accaatgatg ttgatcgcgt tgtcttcgcc gcaggtgaag ggtactaac gctggtcgat 420
tcactggtca tggggtgtgc ggtattgatt gttatgagca cccaaatcag ctggcaatta 480
acactgttat cgctattacc gatgcccatc atggcgatag tgattaagta ttacggtgac 540
caacttcatc agcgttttaa atccgctcag ggtgcctttt ctttgcttaa taatcaggct 600
caagagagcc tgaccagtat tcgcatgatt aaggcctttg gtctggaaga tcgtcagtca 660
caacagtttg ctcaggtagc ggcagaaacc ggtgcgaaga atatgtatgt cgcccgcatt 720
gatgcccgct ttgaccctac aatttatatt gctattggta tcgctaattt attagctatt 780
ggtggcggta gctggatggt ggtgaataac agcattacct tagggcaatt aaccagtttt 840
gttatgtatt tggggctgat gatttggcca atgctggcat tggcatggat gtttaatatt 900
gttgagcgcg gtagtgccgc ttatagccgc atccgcagtt tgttggatga agcacctgtg 960
gttaaagatg gccacattac tttgtctgat gtgcgtgaca cattagcggt taatattcgt 1020
catttttgtt atccaggcag tgatcaaccg gcactacata atgtggtact gacgctggtt 1080
ccaggggcca tgctggggtt atgtgggcca acaggttcgg gtaagagtac cttgctggcc 1140
ttaatccagc ggcaatttga tattgatgac ggtgttattt gttatcaagg gcatccgctg 1200
tcggatattc ggttgaatga ttggcgtggc cgtttatcgg tcgttagcca gacccctttc 1260
ctgttctccg atacggtggc cggtaatatt gccttgggta aacccgatgc gacccccgca 1320
cagattgagc aggcggcccg cctggcctgt gtacatgaag atattttgcg tctgccgcag 1380
ggttatgaca ctgaagtagg cgagcgtgga gtgatgttgt ccggtggaca gaaacagcgc 1440
atatctattg ccagagcgct tttgttggat gctgaaatac ttattcttga tgatgcactt 1500
tctgcggttg atggccagac ggagcatgaa attttaaaaa acctacgcga gtggggcgaa 1560
cagcgtaccg tcattatcag cgcgcatcgc ctttctgcat tgactgaagc cagcgaaatt 1620
ctggtgatgc aacatggtgg tgtaatgcag cgggggcccc acagccttct agtcaatcag 1680
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acgggttggt atcgggagat gtaccgctat cagcaattag aagccgcatt ggatgacggt 1740
gagcaggagg tcgaagccga tgaataacgt tcagcaactt tggccgacat tgaaacgcct 1800
gctttcctac ggttcgcctt atcgtaaacc gctggggctg gcagtcttaa tgctgtgggt 1860
tgcggcggca gcagaggtaa gtggtccact actgatcagt tattttattg accatgtagt 1920
cgccaaaggc acattacctc tggggctagt cagtgggttg gcattggcct atctgttgtt 1980
gcaattattg gccgcgacat tgcactattt tcaggcattg ctgtttaacc gtgcggcagt 2040
gggggtcgtt cagcggctac gcattgatgt gatggacgct gcattacgtc aacctctcag 2100
tgcttttgat actcagcctg ttgggcagtt aatttcccga gtaaccaatg acaccgaagt 2160
gatcaaagat ttatatgtca tggtggtttc tacggttttg aaaagtgcgg ccttaattag 2220
tgcgatgctg gtggcaatgt ttagtctgga ttggcggatg gcgctgattt caatttgtat 2280
cttccctgcg gtgttggtgg tgatgacaat ctatcagcgc tatagcaccc ctatcgttcg 2340
ccgggtacga tcctatctgg ctgatattaa cgatggtttt aatgaagtca ttaatggtat 2400
gggcgtcatt cagcaattcc gtcagcaggc ccgtttcgga gaacgcatgg cgtctgccag 2460
ccgtgcgcat tatgttgccc ggatgcaaac cttacggctg gagggctttc tattacgccc 2520
tttattgagc ctattctctg ccttggtgct atgtggtcta ctgctgcttt tcggtttcag 2580
ccctgaaggt tctgtggggg taggtgtgct gtatgcgttc attaattacc ttggccgcct 2640
gaatgagccg ttgattgaac tgacatcgca gcaatcaatt atgcaacagg ccgtagtggc 2700
aggagagcgt attttgatc tgatggatcg tgcgcagcag ggctatggta gcgacaatat 2760
tcccttgagc agtggccgta ttcaggtgga aaacgtcagc tttgcgtatc gctcggataa 2820
aatggtgtta cacaatattt ctctcaatgt cccctcccgt ggattcgtgg ctttagttgg 2880
gcacaccggc agtggtaaaa gtacgctagc taacctgttg atgggctact atcccgttca 2940
gcaaggtgag attttgcttg atggccggcc attatcccgc ctctcccatc aggttctgcg 3000
ccaggggggta gcgttggtac agcaagatcc cgtggtgttg gctgactcct tctttgcgaa 3060
tatcaccctt gggcgtgacc ttagtgaaca gcaagtgtgg gaggcactcg aaaccgttca 3120
attggcaccg ttggttcgta ccttacctga tggcttgtac agtttacttg gggaacaggg 3180
caataccttg tctgttgggc aaaaacagtt gctggcgatg gcgcgggtgt tggtgcaagc 3240
gccccaaatc ctgattctgg atgaagccac tgcgaatatt gactctggca ctgaacaggc 3300
tattcagcgg gcattacagg tgattcgaaa aaataccacg ctggtggtta ttgctcatcg 3360
cctttcgacg attgtggagg cggatagtat tttggtactg caccgtggtg ttgcggttga 3420
gcagggtaat catcaagcgc tgctagctgc ccgtgggcgt tattaccaga tgtaccagtt 3480
gcagttagtc agcgaagatt tggctgccat tgatcaggaa gctattgata aaggctctat 3540
tgatcaaagt actattgatc aagccggaat gagcgtgagt taa 3583

<210> 36
<211> 624
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(624)

<400> 36
atg ttt aaa cgt cta ttc atg gtc gca ttg ttg gcc ata gca cca ctg 48
Met Phe Lys Arg Leu Phe Met Val Ala Leu Leu Ala Ile Ala Pro Leu
1 5 10 15

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gtt cat gct gtc gat caa agc aac cct tat cgt ctg atg gat gag gca     96
Val His Ala Val Asp Gln Ser Asn Pro Tyr Arg Leu Met Asp Glu Ala
            20                  25                  30

gcg aag aaa acc ttt acg cgt ctg aaa aat gag cag cct aag att aag    144
Ala Lys Lys Thr Phe Thr Arg Leu Lys Asn Glu Gln Pro Lys Ile Lys
        35                  40                  45

caa aat cca gat tat ctc cgc acc att gta cgc gaa gag ctg ttg ccg    192
Gln Asn Pro Asp Tyr Leu Arg Thr Ile Val Arg Glu Glu Leu Leu Pro
    50                  55                  60

ttt gtt cag atc aaa tac gcc ggc gcg tta gta ctg ggt agc tat tat    240
Phe Val Gln Ile Lys Tyr Ala Gly Ala Leu Val Leu Gly Ser Tyr Tyr
65                  70                  75                  80

aaa gat gct aca cct gca cag cgt gaa gcg tat ttc aat gca ttc ggt    288
Lys Asp Ala Thr Pro Ala Gln Arg Glu Ala Tyr Phe Asn Ala Phe Gly
                85                  90                  95

aaa tat ctg gag cag gca tac ggg cag gca ttg gcg ttg tat cac ggc    336
Lys Tyr Leu Glu Gln Ala Tyr Gly Gln Ala Leu Ala Leu Tyr His Gly
            100                 105                 110

caa act tac gat gtg gca cca gac cag cct tta ggg gat gcc aac atc    384
Gln Thr Tyr Asp Val Ala Pro Asp Gln Pro Leu Gly Asp Ala Asn Ile
        115                 120                 125

gtt gct atc cgc gtc acc att ctc gat cca agt ggg cgt cca cct gtc    432
Val Ala Ile Arg Val Thr Ile Leu Asp Pro Ser Gly Arg Pro Pro Val
    130                 135                 140

cgg tta gat ttc caa tgg cgt aaa aat agc caa acc ggt aac tgg cag    480
Arg Leu Asp Phe Gln Trp Arg Lys Asn Ser Gln Thr Gly Asn Trp Gln
145                 150                 155                 160

gct tat gac atg atc gcc gaa ggg gtg agc atg att agc acc aaa cag    528
Ala Tyr Asp Met Ile Ala Glu Gly Val Ser Met Ile Ser Thr Lys Gln
                165                 170                 175

aat gaa tgg gcc tct atc ctg cgc caa aag ggt gtg gat ggt ttg acc    576
Asn Glu Trp Ala Ser Ile Leu Arg Gln Lys Gly Val Asp Gly Leu Thr
            180                 185                 190

caa caa ttg ctg agt gcg gct aaa cag cca atc acc tta gat aaa tag    624
Gln Gln Leu Leu Ser Ala Ala Lys Gln Pro Ile Thr Leu Asp Lys
        195                 200                 205
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<210> 37
<211> 207
<212> PRT
<213> Yersinia pestis

<400> 37
Met Phe Lys Arg Leu Phe Met Val Ala Leu Leu Ala Ile Ala Pro Leu
 1               5                  10                  15

Val His Ala Val Asp Gln Ser Asn Pro Tyr Arg Leu Met Asp Glu Ala
            20                  25                  30

Ala Lys Lys Thr Phe Thr Arg Leu Lys Asn Glu Gln Pro Lys Ile Lys
        35                  40                  45

Gln Asn Pro Asp Tyr Leu Arg Thr Ile Val Arg Glu Glu Leu Leu Pro
    50                  55                  60

Phe Val Gln Ile Lys Tyr Ala Gly Ala Leu Val Leu Gly Ser Tyr Tyr
65                  70                  75                  80

Lys Asp Ala Thr Pro Ala Gln Arg Glu Ala Tyr Phe Asn Ala Phe Gly
                85                  90                  95

Lys Tyr Leu Glu Gln Ala Tyr Gly Gln Ala Leu Ala Leu Tyr His Gly
            100                 105                 110

Gln Thr Tyr Asp Val Ala Pro Asp Gln Pro Leu Gly Asp Ala Asn Ile
        115                 120                 125

Val Ala Ile Arg Val Thr Ile Leu Asp Pro Ser Gly Arg Pro Pro Val
    130                 135                 140

Arg Leu Asp Phe Gln Trp Arg Lys Asn Ser Gln Thr Gly Asn Trp Gln
145                 150                 155                 160

Ala Tyr Asp Met Ile Ala Glu Gly Val Ser Met Ile Ser Thr Lys Gln
                165                 170                 175

Asn Glu Trp Ala Ser Ile Leu Arg Gln Lys Gly Val Asp Gly Leu Thr
            180                 185                 190

Gln Gln Leu Leu Ser Ala Ala Lys Gln Pro Ile Thr Leu Asp Lys
        195                 200                 205
```

<210> 38
<211> 1455
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(1455)

<400> 38
atg caa act gat gtc gtt ctg ccg tta gtc ggc tat ctg gtg ttg gtc 48
Met Gln Thr Asp Val Val Leu Pro Leu Val Gly Tyr Leu Val Leu Val
1 5 10 15

ttt ggc tta tct att tat gct tat acg cgc cgc caa acc ggg aat ttt 96
Phe Gly Leu Ser Ile Tyr Ala Tyr Thr Arg Arg Gln Thr Gly Asn Phe
20 25 30

ctc aac gaa tat ttt atc ggc aac cgt tcg atg ggc ggt ttt gta ttg 144
Leu Asn Glu Tyr Phe Ile Gly Asn Arg Ser Met Gly Gly Phe Val Leu
35 40 45

gcg atg acc ctg acc gcc acc tat atc agc gcc agc tcg ttt att ggt 192
Ala Met Thr Leu Thr Ala Thr Tyr Ile Ser Ala Ser Ser Phe Ile Gly
50 55 60

gga cca ggt gcc gct tat aaa tac ggc ctt ggc tgg gtc tta ctg gcg 240
Gly Pro Gly Ala Ala Tyr Lys Tyr Gly Leu Gly Trp Val Leu Leu Ala
65 70 75 80

atg atc caa ttg cct gcg gtc tgg ctt tcc ctc ggt gtc tta ggc aaa 288
Met Ile Gln Leu Pro Ala Val Trp Leu Ser Leu Gly Val Leu Gly Lys
85 90 95

aag ttt gcc att ctg gcg cgt cgc tat aat gcc gtg acc ctc aac gat 336
Lys Phe Ala Ile Leu Ala Arg Arg Tyr Asn Ala Val Thr Leu Asn Asp
100 105 110

atg ttg tat gcc cgt tat cag agc cgt tta ctg gtt tgg ctg gcc agt 384
Met Leu Tyr Ala Arg Tyr Gln Ser Arg Leu Leu Val Trp Leu Ala Ser
115 120 125

atc agc ctg ctg gtg gct ttt gtc ggt gcc atg acc gtg caa ttt att 432
Ile Ser Leu Leu Val Ala Phe Val Gly Ala Met Thr Val Gln Phe Ile
130 135 140

ggt ggc gca cgg ttg tta gaa acg gcg gcg ggg atc cct tac gac act 480
Gly Gly Ala Arg Leu Leu Glu Thr Ala Ala Gly Ile Pro Tyr Asp Thr

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145                 150                 155                 160

ggc tta ttg att ttt ggt atc agt atc gcc ctg tac acc tcg ttt ggt     528
Gly Leu Leu Ile Phe Gly Ile Ser Ile Ala Leu Tyr Thr Ser Phe Gly
                165                 170                 175

ggc ttc cgg gcc agt gtc ttg aat gat gcc ctg caa ggg tta gtg atg     576
Gly Phe Arg Ala Ser Val Leu Asn Asp Ala Leu Gln Gly Leu Val Met
            180                 185                 190

ctg atc ggc acc att tta ctg tta gtt gcg gtg atc cac gcg gca ggt     624
Leu Ile Gly Thr Ile Leu Leu Leu Val Ala Val Ile His Ala Ala Gly
        195                 200                 205

ggc cta cac aaa gcc gtc gaa acg ctg caa cat atc gat ccg gcg ctg     672
Gly Leu His Lys Ala Val Glu Thr Leu Gln His Ile Asp Pro Ala Leu
    210                 215                 220

gtt tcc ccc caa ggc ggc gat cag atc ctc gac gtg cca ttt atg gct     720
Val Ser Pro Gln Gly Gly Asp Gln Ile Leu Asp Val Pro Phe Met Ala
225                 230                 235                 240

tcg ttc tgg atc ctg gtc tgt ttt ggg gtg att ggt ctg cca cac acc     768
Ser Phe Trp Ile Leu Val Cys Phe Gly Val Ile Gly Leu Pro His Thr
                245                 250                 255

gcc gta cgt tgt att tcg tat cgt gac agt aaa gcg gtt cat cgc ggt     816
Ala Val Arg Cys Ile Ser Tyr Arg Asp Ser Lys Ala Val His Arg Gly
            260                 265                 270

att atc ctc ggc acc atc gtg gtg gcg atc cta atg ttc ggt atg cac     864
Ile Ile Leu Gly Thr Ile Val Val Ala Ile Leu Met Phe Gly Met His
        275                 280                 285

ctg gct ggc gca ctg ggg cgg gcg gtg tta cca gat ctg aaa att cca     912
Leu Ala Gly Ala Leu Gly Arg Ala Val Leu Pro Asp Leu Lys Ile Pro
    290                 295                 300

gat caa gta atc ccg aca ctg atg atc acc gta ctg ccg cca ttt gct     960
Asp Gln Val Ile Pro Thr Leu Met Ile Thr Val Leu Pro Pro Phe Ala
305                 310                 315                 320

gcg ggg ata ttc ctg gca gca ccg atg gcg gcg atc atg tcg acc atc     1008
Ala Gly Ile Phe Leu Ala Ala Pro Met Ala Ala Ile Met Ser Thr Ile
                325                 330                 335

aat gcc cag tta ctg caa tct tct gct acc atc gtg aag gat ttg tat     1056
Asn Ala Gln Leu Leu Gln Ser Ser Ala Thr Ile Val Lys Asp Leu Tyr
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            340                 345                 350

ctc aat ctg tgg cca gca gag tta aag aat gag cgc aag ctg gca cgt   1104
Leu Asn Leu Trp Pro Ala Glu Leu Lys Asn Glu Arg Lys Leu Ala Arg
        355                 360                 365

atc tcc agc tta tcc aca ctc att ctt ggg cta tta ttg ctc ttg gcc   1152
Ile Ser Ser Leu Ser Thr Leu Ile Leu Gly Leu Leu Leu Leu Leu Ala
    370                 375                 380

gcc tgg cga cca cct gaa atg att atc tgg ttg aac cta ctg gcc ttt   1200
Ala Trp Arg Pro Pro Glu Met Ile Ile Trp Leu Asn Leu Leu Ala Phe
385                 390                 395                 400

ggc gga ctg gaa gcg gta ttc ctc tgg cca ttg gta ttg gga tta tac   1248
Gly Gly Leu Glu Ala Val Phe Leu Trp Pro Leu Val Leu Gly Leu Tyr
                405                 410                 415

tgg gag cga gcc aat gcc cac ggc gct ctt agc gcc atg atc gtc ggt   1296
Trp Glu Arg Ala Asn Ala His Gly Ala Leu Ser Ala Met Ile Val Gly
            420                 425                 430

gcg gta tgc tat acg gta tta gcc agc ttc gac atc aag ata gcc ggc   1344
Ala Val Cys Tyr Thr Val Leu Ala Ser Phe Asp Ile Lys Ile Ala Gly
        435                 440                 445

ctg cac ccc att gtg ccg tca ctt aca ctt aat ctg ttg gcg ttt tat   1392
Leu His Pro Ile Val Pro Ser Leu Thr Leu Asn Leu Leu Ala Phe Tyr
    450                 455                 460

atc ggt aat ctg ttt ggc gac aga gcg cgg gcg cga cac ccc gcc atc   1440
Ile Gly Asn Leu Phe Gly Asp Arg Ala Arg Ala Arg His Pro Ala Ile
465                 470                 475                 480

gtc agt gcc gat taa                                               1455
Val Ser Ala Asp
                485


<210> 39
<211> 484
<212> PRT
<213> Yersinia pestis

<400> 39
Met Gln Thr Asp Val Val Leu Pro Leu Val Gly Tyr Leu Val Leu Val
  1               5                  10                  15
```

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Phe Gly Leu Ser Ile Tyr Ala Tyr Thr Arg Arg Gln Thr Gly Asn Phe
            20                  25                  30

Leu Asn Glu Tyr Phe Ile Gly Asn Arg Ser Met Gly Gly Phe Val Leu
        35                  40                  45

Ala Met Thr Leu Thr Ala Thr Tyr Ile Ser Ala Ser Ser Phe Ile Gly
    50                  55                  60

Gly Pro Gly Ala Ala Tyr Lys Tyr Gly Leu Gly Trp Val Leu Leu Ala
65                  70                  75                  80

Met Ile Gln Leu Pro Ala Val Trp Leu Ser Leu Gly Val Leu Gly Lys
                85                  90                  95

Lys Phe Ala Ile Leu Ala Arg Arg Tyr Asn Ala Val Thr Leu Asn Asp
            100                 105                 110

Met Leu Tyr Ala Arg Tyr Gln Ser Arg Leu Leu Val Trp Leu Ala Ser
        115                 120                 125

Ile Ser Leu Leu Val Ala Phe Val Gly Ala Met Thr Val Gln Phe Ile
    130                 135                 140

Gly Gly Ala Arg Leu Leu Glu Thr Ala Ala Gly Ile Pro Tyr Asp Thr
145                 150                 155                 160

Gly Leu Leu Ile Phe Gly Ile Ser Ile Ala Leu Tyr Thr Ser Phe Gly
                165                 170                 175

Gly Phe Arg Ala Ser Val Leu Asn Asp Ala Leu Gln Gly Leu Val Met
            180                 185                 190

Leu Ile Gly Thr Ile Leu Leu Leu Val Ala Val Ile His Ala Ala Gly
        195                 200                 205

Gly Leu His Lys Ala Val Glu Thr Leu Gln His Ile Asp Pro Ala Leu
    210                 215                 220

Val Ser Pro Gln Gly Gly Asp Gln Ile Leu Asp Val Pro Phe Met Ala
225                 230                 235                 240

Ser Phe Trp Ile Leu Val Cys Phe Gly Val Ile Gly Leu Pro His Thr
                245                 250                 255

Ala Val Arg Cys Ile Ser Tyr Arg Asp Ser Lys Ala Val His Arg Gly
            260                 265                 270
```

Ile Ile Leu Gly Thr Ile Val Val Ala Ile Leu Met Phe Gly Met His
275 280 285

Leu Ala Gly Ala Leu Gly Arg Ala Val Leu Pro Asp Leu Lys Ile Pro
290 295 300

Asp Gln Val Ile Pro Thr Leu Met Ile Thr Val Leu Pro Pro Phe Ala
305 310 315 320

Ala Gly Ile Phe Leu Ala Ala Pro Met Ala Ala Ile Met Ser Thr Ile
325 330 335

Asn Ala Gln Leu Leu Gln Ser Ser Ala Thr Ile Val Lys Asp Leu Tyr
340 345 350

Leu Asn Leu Trp Pro Ala Glu Leu Lys Asn Glu Arg Lys Leu Ala Arg
355 360 365

Ile Ser Ser Leu Ser Thr Leu Ile Leu Gly Leu Leu Leu Leu Leu Ala
370 375 380

Ala Trp Arg Pro Pro Glu Met Ile Ile Trp Leu Asn Leu Leu Ala Phe
385 390 395 400

Gly Gly Leu Glu Ala Val Phe Leu Trp Pro Leu Val Leu Gly Leu Tyr
405 410 415

Trp Glu Arg Ala Asn Ala His Gly Ala Leu Ser Ala Met Ile Val Gly
420 425 430

Ala Val Cys Tyr Thr Val Leu Ala Ser Phe Asp Ile Lys Ile Ala Gly
435 440 445

Leu His Pro Ile Val Pro Ser Leu Thr Leu Asn Leu Leu Ala Phe Tyr
450 455 460

Ile Gly Asn Leu Phe Gly Asp Arg Ala Arg Ala Arg His Pro Ala Ile
465 470 475 480

Val Ser Ala Asp

<210> 40
<211> 879
<212> DNA
<213> Yersinia pestis

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<220>
<221> CDS
<222> (1)..(879)

<400> 40
atg gcg aga ttt tgg cag ata ctg att gcg tta tta ctg gtg cca aca    48
Met Ala Arg Phe Trp Gln Ile Leu Ile Ala Leu Leu Leu Val Pro Thr
 1               5                   10                  15

ttg gca cag gct gaa gaa gca acg att gaa aag att cat gat gcg ccc    96
Leu Ala Gln Ala Glu Glu Ala Thr Ile Glu Lys Ile His Asp Ala Pro
             20                  25                  30

gca gtg cgt ggc agt att atc gcg gca atg ttg cag gac cac gat aat    144
Ala Val Arg Gly Ser Ile Ile Ala Ala Met Leu Gln Asp His Asp Asn
         35                  40                  45

cct ttc cta ctt tat ccg tat gaa acc aac tat ttg ctc tac acc tat    192
Pro Phe Leu Leu Tyr Pro Tyr Glu Thr Asn Tyr Leu Leu Tyr Thr Tyr
     50                  55                  60

acc aac gag atc aat aaa caa gcc att agc tcg tat gat tgg gct gaa    240
Thr Asn Glu Ile Asn Lys Gln Ala Ile Ser Ser Tyr Asp Trp Ala Glu
 65                  70                  75                  80

cag gcg aat aaa gat gaa gta aaa ttc caa ctg agt tta gct ttc cct    288
Gln Ala Asn Lys Asp Glu Val Lys Phe Gln Leu Ser Leu Ala Phe Pro
                 85                  90                  95

atc tgg cgt ggt att gcc ggg gat aac tca tta ttg ggg gct tct tat    336
Ile Trp Arg Gly Ile Ala Gly Asp Asn Ser Leu Leu Gly Ala Ser Tyr
            100                 105                 110

acc cag cgt tca tgg tgg cag gca tcc aac agt gaa gaa tct tca cct    384
Thr Gln Arg Ser Trp Trp Gln Ala Ser Asn Ser Glu Glu Ser Ser Pro
        115                 120                 125

ttt cgt gaa acc aac tac gag cca cag ctg ttt ttg gcg tgg tca aca    432
Phe Arg Glu Thr Asn Tyr Glu Pro Gln Leu Phe Leu Ala Trp Ser Thr
    130                 135                 140

gat tac gaa ttg gct ggc tgg act ttc cgc gaa gtc gaa ttt ggt ttt    480
Asp Tyr Glu Leu Ala Gly Trp Thr Phe Arg Glu Val Glu Phe Gly Phe
145                 150                 155                 160

aac cat caa tcc aac ggt aaa gct gac cca acc tca cgt agt tgg aac    528
Asn His Gln Ser Asn Gly Lys Ala Asp Pro Thr Ser Arg Ser Trp Asn
                165                 170                 175
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cgt gtt tat acc cgc gtg atg gca caa cgt ggc aat ttg gaa atc gac 576
Arg Val Tyr Thr Arg Val Met Ala Gln Arg Gly Asn Leu Glu Ile Asp
180 185 190

ctg aag cct tgg tat cgt att cct gaa agc gac agt aaa gat gat aac 624
Leu Lys Pro Trp Tyr Arg Ile Pro Glu Ser Asp Ser Lys Asp Asp Asn
195 200 205

cct gat att acg aaa tac atg ggg tat tat cgc ctg aaa gtc ggc tat 672
Pro Asp Ile Thr Lys Tyr Met Gly Tyr Tyr Arg Leu Lys Val Gly Tyr
210 215 220

gcc ctg ggt gac agc gta ttc agc ctt gat ggt cgc tat aac tgg aat 720
Ala Leu Gly Asp Ser Val Phe Ser Leu Asp Gly Arg Tyr Asn Trp Asn
225 230 235 240

acc ggt tac ggt ggc gcg gaa atg ggc tgg agc tac cca att acc aaa 768
Thr Gly Tyr Gly Gly Ala Glu Met Gly Trp Ser Tyr Pro Ile Thr Lys
245 250 255

cat gtt cgc ttc tat act cag gta ttc agt ggc tac ggt gag tca atg 816
His Val Arg Phe Tyr Thr Gln Val Phe Ser Gly Tyr Gly Glu Ser Met
260 265 270

att gac tat aac ttt agg caa aca cgg gtg ggt gta ggt atc atg ttg 864
Ile Asp Tyr Asn Phe Arg Gln Thr Arg Val Gly Val Gly Ile Met Leu
275 280 285

aac gat gtc ctt taa 879
Asn Asp Val Leu
290

<210> 41
<211> 292
<212> PRT
<213> Yersinia pestis

<400> 41
Met Ala Arg Phe Trp Gln Ile Leu Ile Ala Leu Leu Leu Val Pro Thr
1 5 10 15

Leu Ala Gln Ala Glu Glu Ala Thr Ile Glu Lys Ile His Asp Ala Pro
20 25 30

Ala Val Arg Gly Ser Ile Ile Ala Ala Met Leu Gln Asp His Asp Asn
35 40 45

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Pro Phe Leu Leu Tyr Pro Tyr Glu Thr Asn Tyr Leu Leu Tyr Thr Tyr
     50                  55                  60

Thr Asn Glu Ile Asn Lys Gln Ala Ile Ser Ser Tyr Asp Trp Ala Glu
65                  70                  75                  80

Gln Ala Asn Lys Asp Glu Val Lys Phe Gln Leu Ser Leu Ala Phe Pro
                85                  90                  95

Ile Trp Arg Gly Ile Ala Gly Asp Asn Ser Leu Leu Gly Ala Ser Tyr
            100                 105                 110

Thr Gln Arg Ser Trp Trp Gln Ala Ser Asn Ser Glu Glu Ser Ser Pro
        115                 120                 125

Phe Arg Glu Thr Asn Tyr Glu Pro Gln Leu Phe Leu Ala Trp Ser Thr
    130                 135                 140

Asp Tyr Glu Leu Ala Gly Trp Thr Phe Arg Glu Val Glu Phe Gly Phe
145                 150                 155                 160

Asn His Gln Ser Asn Gly Lys Ala Asp Pro Thr Ser Arg Ser Trp Asn
                165                 170                 175

Arg Val Tyr Thr Arg Val Met Ala Gln Arg Gly Asn Leu Glu Ile Asp
            180                 185                 190

Leu Lys Pro Trp Tyr Arg Ile Pro Glu Ser Asp Ser Lys Asp Asp Asn
        195                 200                 205

Pro Asp Ile Thr Lys Tyr Met Gly Tyr Tyr Arg Leu Lys Val Gly Tyr
    210                 215                 220

Ala Leu Gly Asp Ser Val Phe Ser Leu Asp Gly Arg Tyr Asn Trp Asn
225                 230                 235                 240

Thr Gly Tyr Gly Gly Ala Glu Met Gly Trp Ser Tyr Pro Ile Thr Lys
                245                 250                 255

His Val Arg Phe Tyr Thr Gln Val Phe Ser Gly Tyr Gly Glu Ser Met
            260                 265                 270

Ile Asp Tyr Asn Phe Arg Gln Thr Arg Val Gly Val Gly Ile Met Leu
        275                 280                 285

Asn Asp Val Leu
    290
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<210> 42
<211> 2556
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(2556)

<400> 42
atg gag caa ccc cgc ctc tcc ttc ttt gcc agt gtt cgt ggg cga ttg      48
Met Glu Gln Pro Arg Leu Ser Phe Phe Ala Ser Val Arg Gly Arg Leu
  1               5                  10                  15

ttg ttc ttc aac ttg ctc gtg gtg gcg gtc acc ctg atg gtg agt ggt      96
Leu Phe Phe Asn Leu Leu Val Val Ala Val Thr Leu Met Val Ser Gly
             20                  25                  30

gtc gcg gtg ctg ggc ttc gag cag gca agc cgc tta caa aag cag gtc     144
Val Ala Val Leu Gly Phe Glu Gln Ala Ser Arg Leu Gln Lys Gln Val
         35                  40                  45

cag gag cgg aca ctg cgc gat atg tca agc agc atg gcg ctg gcg cgc     192
Gln Glu Arg Thr Leu Arg Asp Met Ser Ser Ser Met Ala Leu Ala Arg
     50                  55                  60

gat acc gca aat gtg gcg acg gcg gcg gtg cgg ctt tcc caa gtg gtt     240
Asp Thr Ala Asn Val Ala Thr Ala Ala Val Arg Leu Ser Gln Val Val
 65                  70                  75                  80

ggg gcg ctt gaa ttc cag agt gaa gcg gcc agt ctt caa gag acg caa     288
Gly Ala Leu Glu Phe Gln Ser Glu Ala Ala Ser Leu Gln Glu Thr Gln
                 85                  90                  95

ctg gcg tta cga agt tca ctc gct cat ctt gct aat gcc ccg ctt gcc     336
Leu Ala Leu Arg Ser Ser Leu Ala His Leu Ala Asn Ala Pro Leu Ala
            100                 105                 110

agc cat gaa ccg cta ttg gtg aaa cgt atc att gag cgt agc aat gaa     384
Ser His Glu Pro Leu Leu Val Lys Arg Ile Ile Glu Arg Ser Asn Glu
        115                 120                 125

ctg gaa acc agc gtt gca cgt atg ctg aat ttg ggt cac cgt cgc cat     432
Leu Glu Thr Ser Val Ala Arg Met Leu Asn Leu Gly His Arg Arg His
    130                 135                 140
```

```
ctt gag cgt aac ctg ctg ctg agc gcc ctc tat cag acc caa agt tat     480
Leu Glu Arg Asn Leu Leu Leu Ser Ala Leu Tyr Gln Thr Gln Ser Tyr
145                 150                 155                 160

ctt cac cat ctg cag gag att aac cag cgc gat ggg ctg aac aaa ccc     528
Leu His His Leu Gln Glu Ile Asn Gln Arg Asp Gly Leu Asn Lys Pro
                165                 170                 175

gat gcc gca ctg cta aaa gag atg gat cgc ctg cta ctg gtg gct atc     576
Asp Ala Ala Leu Leu Lys Glu Met Asp Arg Leu Leu Leu Val Ala Ile
            180                 185                 190

cag acc tcc tcg ccc aaa gct gcc gta cag caa ctt act gag gtg atg     624
Gln Thr Ser Ser Pro Lys Ala Ala Val Gln Gln Leu Thr Glu Val Met
        195                 200                 205

cag gca ttg cct gcc cat gct gac tcg ccg ctg gtg gag gaa atc ttg     672
Gln Ala Leu Pro Ala His Ala Asp Ser Pro Leu Val Glu Glu Ile Leu
    210                 215                 220

caa gag ttc agc gcc agc ctg tat cag ctg ctg ccg ttg tcc atc acg     720
Gln Glu Phe Ser Ala Ser Leu Tyr Gln Leu Leu Pro Leu Ser Ile Thr
225                 230                 235                 240

ctt gaa aat agc gat ctg agc att acc tgg tac atg tac cac gtc aaa     768
Leu Glu Asn Ser Asp Leu Ser Ile Thr Trp Tyr Met Tyr His Val Lys
                245                 250                 255

gcg ttg gtg gcg ttt ctc aat cag ggc atc aat atc tat gta caa aag     816
Ala Leu Val Ala Phe Leu Asn Gln Gly Ile Asn Ile Tyr Val Gln Lys
            260                 265                 270

gtg ggg gag gaa tcg ctg cag cgt agc caa caa aac cac aaa gcc ttg     864
Val Gly Glu Glu Ser Leu Gln Arg Ser Gln Gln Asn His Lys Ala Leu
        275                 280                 285

caa tcg atc atc acg tct att ggt ctg ttt gcc ctg ttg gca ctg gtt     912
Gln Ser Ile Ile Thr Ser Ile Gly Leu Phe Ala Leu Leu Ala Leu Val
    290                 295                 300

atc acc ggg ttt gcc ggc tgg tat atc tac cat aac ctt ggc tct aac     960
Ile Thr Gly Phe Ala Gly Trp Tyr Ile Tyr His Asn Leu Gly Ser Asn
305                 310                 315                 320

tta acg gcg ata tct cat gcc atg acc cga ttg gca aga gga gaa aaa     1008
Leu Thr Ala Ile Ser His Ala Met Thr Arg Leu Ala Arg Gly Glu Lys
                325                 330                 335
```

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gag gtc agc gta cca gcc caa caa cgg cgt gat gaa ctg ggc gaa ctg     1056
Glu Val Ser Val Pro Ala Gln Gln Arg Arg Asp Glu Leu Gly Glu Leu
            340                 345                 350

gct cgc gcg ttt aac gtt ttt gcc cgc aat acc gct tcg ctg gag cag     1104
Ala Arg Ala Phe Asn Val Phe Ala Arg Asn Thr Ala Ser Leu Glu Gln
        355                 360                 365

aca tca cgt ctt ctg aaa gag aaa agt acg cta ttg gaa acc acc ttt     1152
Thr Ser Arg Leu Leu Lys Glu Lys Ser Thr Leu Leu Glu Thr Thr Phe
    370                 375                 380

cac gct atg cgc gat ggt ttt gcc ctg ttc gac aac gag ggc ttt ctg     1200
His Ala Met Arg Asp Gly Phe Ala Leu Phe Asp Asn Glu Gly Phe Leu
385                 390                 395                 400

gtg gtg tgg aac ccg caa tac cca ctg ttg ctg ggg ctg gca ccg gag     1248
Val Val Trp Asn Pro Gln Tyr Pro Leu Leu Leu Gly Leu Ala Pro Glu
                405                 410                 415

cag cta cag cat ggt cag cac tac ctt caa tta ttg aag cag atg acg     1296
Gln Leu Gln His Gly Gln His Tyr Leu Gln Leu Leu Lys Gln Met Thr
            420                 425                 430

cca ctg caa gag cat ata ctt gag aac ctc gcc ctc ccg ctg cca aaa     1344
Pro Leu Gln Glu His Ile Leu Glu Asn Leu Ala Leu Pro Leu Pro Lys
        435                 440                 445

acc caa gag cta aga ctt gag gac cat cgc act atc gaa ctg cgt ttc     1392
Thr Gln Glu Leu Arg Leu Glu Asp His Arg Thr Ile Glu Leu Arg Phe
    450                 455                 460

agt ccg gtt cct gga cga ggg atg gtt aat gtg gtg ttg gat cgt agc     1440
Ser Pro Val Pro Gly Arg Gly Met Val Asn Val Val Leu Asp Arg Ser
465                 470                 475                 480

gag cgc aaa gca ctg gaa gaa gcg ctg gtc cat agc caa aaa atg aag     1488
Glu Arg Lys Ala Leu Glu Glu Ala Leu Val His Ser Gln Lys Met Lys
                485                 490                 495

gcg gta ggg cag ctc acg ggc ggc ctg gct cat gat ttt aat aac ctg     1536
Ala Val Gly Gln Leu Thr Gly Gly Leu Ala His Asp Phe Asn Asn Leu
            500                 505                 510

ctg gcg gtg att att ggc agt ctt gag cta acc gct acg gac tcg tcg     1584
Leu Ala Val Ile Ile Gly Ser Leu Glu Leu Thr Ala Thr Asp Ser Ser
        515                 520                 525
```

gat gcc acg cgt att cat cgt gct ctg aag gcc gct gag cgg ggg gcg 1632
Asp Ala Thr Arg Ile His Arg Ala Leu Lys Ala Ala Glu Arg Gly Ala
530 535 540

caa ctc acc caa cgg ttg ctg gcg ttc tca cgc aag cag tcg ctt cac 1680
Gln Leu Thr Gln Arg Leu Leu Ala Phe Ser Arg Lys Gln Ser Leu His
545 550 555 560

cct cga gct gtt gcg atg aaa gaa cta ctt gat aac ctg gac ccg ctg 1728
Pro Arg Ala Val Ala Met Lys Glu Leu Leu Asp Asn Leu Asp Pro Leu
565 570 575

ata cgc cac tcg ctt ccg gct cat ctt acg ctc aca att gaa gct cag 1776
Ile Arg His Ser Leu Pro Ala His Leu Thr Leu Thr Ile Glu Ala Gln
580 585 590

cag cct gcc tgg cac gcc tgg ata gac gta aac caa ctg gaa aac gca 1824
Gln Pro Ala Trp His Ala Trp Ile Asp Val Asn Gln Leu Glu Asn Ala
595 600 605

att atc aat ctg gtg atg aat gct cgc gac gcg atg gaa ggg cgc agc 1872
Ile Ile Asn Leu Val Met Asn Ala Arg Asp Ala Met Glu Gly Arg Ser
610 615 620

ggc gag att aaa atc cgc acc tgg aat caa cgc gta gag cgt ggt gaa 1920
Gly Glu Ile Lys Ile Arg Thr Trp Asn Gln Arg Val Glu Arg Gly Glu
625 630 635 640

ggg cgc aaa caa gat atg gtg gtg ctg gaa gtg gct gat agc ggc cat 1968
Gly Arg Lys Gln Asp Met Val Val Leu Glu Val Ala Asp Ser Gly His
645 650 655

ggc atg acc acc gca gtg aaa gag cag gtt ttt gaa ccc ttc ttc acc 2016
Gly Met Thr Thr Ala Val Lys Glu Gln Val Phe Glu Pro Phe Phe Thr
660 665 670

acc aag caa acc ggt agc ggg agt ggg ctt ggg ctg tca atg gta tac 2064
Thr Lys Gln Thr Gly Ser Gly Ser Gly Leu Gly Leu Ser Met Val Tyr
675 680 685

ggc ttt gtg cgc cag tcc gga ggg cgg gta cag ata gaa agt gaa ccg 2112
Gly Phe Val Arg Gln Ser Gly Gly Arg Val Gln Ile Glu Ser Glu Pro
690 695 700

ggg aaa ggg acc cgg gtc tgc ttg cag tta ccc cgt gca ctc aca caa 2160
Gly Lys Gly Thr Arg Val Cys Leu Gln Leu Pro Arg Ala Leu Thr Gln
705 710 715 720

agt ctg ata gaa gtc ctg cca gcg ctt ggt gcc gtt gcg aat atg gct 2208
Ser Leu Ile Glu Val Leu Pro Ala Leu Gly Ala Val Ala Asn Met Ala
725 730 735

gat cag cta gtc tta gtg ctg gaa gat gag ccg gat gta cgc cag acc 2256
Asp Gln Leu Val Leu Val Leu Glu Asp Glu Pro Asp Val Arg Gln Thr
740 745 750

ctg tgc gag caa ctc cat caa ctg ggc tac ctg acg ctt gaa acc ggc 2304
Leu Cys Glu Gln Leu His Gln Leu Gly Tyr Leu Thr Leu Glu Thr Gly
755 760 765

gac agt cgg cag gcg ctg gca ttg atg gcc gac gtg ccg gat atc agc 2352
Asp Ser Arg Gln Ala Leu Ala Leu Met Ala Asp Val Pro Asp Ile Ser
770 775 780

att gtg ata agc gac tta atg cta ccc ggc gac atg acc ggt gcg gaa 2400
Ile Val Ile Ser Asp Leu Met Leu Pro Gly Asp Met Thr Gly Ala Glu
785 790 795 800

gtg ctt cag caa gcg cgc agt gtt tat cct cat ctt aag ctg ttg tta 2448
Val Leu Gln Gln Ala Arg Ser Val Tyr Pro His Leu Lys Leu Leu Leu
805 810 815

att agt ggc cag gat ctg cgg cgc agc aag aat ttc atg ccg gag gtg 2496
Ile Ser Gly Gln Asp Leu Arg Arg Ser Lys Asn Phe Met Pro Glu Val
820 825 830

gaa ctg ctg cgt aag cct ttt aac caa caa cag cta gta cag gcg ctg 2544
Glu Leu Leu Arg Lys Pro Phe Asn Gln Gln Gln Leu Val Gln Ala Leu
835 840 845

caa aga gtc tga 2556
Gln Arg Val
850

<210> 43
<211> 851
<212> PRT
<213> Yersinia pestis

<400> 43
Met Glu Gln Pro Arg Leu Ser Phe Phe Ala Ser Val Arg Gly Arg Leu
1 5 10 15

Leu Phe Phe Asn Leu Leu Val Val Ala Val Thr Leu Met Val Ser Gly

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            20                  25                  30

Val Ala Val Leu Gly Phe Glu Gln Ala Ser Arg Leu Gln Lys Gln Val
        35                  40                  45

Gln Glu Arg Thr Leu Arg Asp Met Ser Ser Ser Met Ala Leu Ala Arg
    50                  55                  60

Asp Thr Ala Asn Val Ala Thr Ala Ala Val Arg Leu Ser Gln Val Val
65                  70                  75                  80

Gly Ala Leu Glu Phe Gln Ser Glu Ala Ala Ser Leu Gln Glu Thr Gln
                85                  90                  95

Leu Ala Leu Arg Ser Ser Leu Ala His Leu Ala Asn Ala Pro Leu Ala
            100                 105                 110

Ser His Glu Pro Leu Leu Val Lys Arg Ile Ile Glu Arg Ser Asn Glu
        115                 120                 125

Leu Glu Thr Ser Val Ala Arg Met Leu Asn Leu Gly His Arg Arg His
    130                 135                 140

Leu Glu Arg Asn Leu Leu Leu Ser Ala Leu Tyr Gln Thr Gln Ser Tyr
145                 150                 155                 160

Leu His His Leu Gln Glu Ile Asn Gln Arg Asp Gly Leu Asn Lys Pro
                165                 170                 175

Asp Ala Ala Leu Leu Lys Glu Met Asp Arg Leu Leu Leu Val Ala Ile
            180                 185                 190

Gln Thr Ser Ser Pro Lys Ala Ala Val Gln Gln Leu Thr Glu Val Met
        195                 200                 205

Gln Ala Leu Pro Ala His Ala Asp Ser Pro Leu Val Glu Glu Ile Leu
    210                 215                 220

Gln Glu Phe Ser Ala Ser Leu Tyr Gln Leu Leu Pro Leu Ser Ile Thr
225                 230                 235                 240

Leu Glu Asn Ser Asp Leu Ser Ile Thr Trp Tyr Met Tyr His Val Lys
                245                 250                 255

Ala Leu Val Ala Phe Leu Asn Gln Gly Ile Asn Ile Tyr Val Gln Lys
            260                 265                 270

Val Gly Glu Glu Ser Leu Gln Arg Ser Gln Gln Asn His Lys Ala Leu
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        275                 280                 285

Gln Ser Ile Ile Thr Ser Ile Gly Leu Phe Ala Leu Leu Ala Leu Val
    290                 295                 300

Ile Thr Gly Phe Ala Gly Trp Tyr Ile Tyr His Asn Leu Gly Ser Asn
305                 310                 315                 320

Leu Thr Ala Ile Ser His Ala Met Thr Arg Leu Ala Arg Gly Glu Lys
                325                 330                 335

Glu Val Ser Val Pro Ala Gln Gln Arg Arg Asp Glu Leu Gly Glu Leu
            340                 345                 350

Ala Arg Ala Phe Asn Val Phe Ala Arg Asn Thr Ala Ser Leu Glu Gln
        355                 360                 365

Thr Ser Arg Leu Leu Lys Glu Lys Ser Thr Leu Leu Glu Thr Thr Phe
    370                 375                 380

His Ala Met Arg Asp Gly Phe Ala Leu Phe Asp Asn Glu Gly Phe Leu
385                 390                 395                 400

Val Val Trp Asn Pro Gln Tyr Pro Leu Leu Leu Gly Leu Ala Pro Glu
                405                 410                 415

Gln Leu Gln His Gly Gln His Tyr Leu Gln Leu Leu Lys Gln Met Thr
            420                 425                 430

Pro Leu Gln Glu His Ile Leu Glu Asn Leu Ala Leu Pro Leu Pro Lys
        435                 440                 445

Thr Gln Glu Leu Arg Leu Glu Asp His Arg Thr Ile Glu Leu Arg Phe
    450                 455                 460

Ser Pro Val Pro Gly Arg Gly Met Val Asn Val Val Leu Asp Arg Ser
465                 470                 475                 480

Glu Arg Lys Ala Leu Glu Glu Ala Leu Val His Ser Gln Lys Met Lys
                485                 490                 495

Ala Val Gly Gln Leu Thr Gly Gly Leu Ala His Asp Phe Asn Asn Leu
            500                 505                 510

Leu Ala Val Ile Ile Gly Ser Leu Glu Leu Thr Ala Thr Asp Ser Ser
        515                 520                 525

Asp Ala Thr Arg Ile His Arg Ala Leu Lys Ala Ala Glu Arg Gly Ala
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530 535 540

Gln Leu Thr Gln Arg Leu Leu Ala Phe Ser Arg Lys Gln Ser Leu His
545 550 555 560

Pro Arg Ala Val Ala Met Lys Glu Leu Leu Asp Asn Leu Asp Pro Leu
565 570 575

Ile Arg His Ser Leu Pro Ala His Leu Thr Leu Thr Ile Glu Ala Gln
580 585 590

Gln Pro Ala Trp His Ala Trp Ile Asp Val Asn Gln Leu Glu Asn Ala
595 600 605

Ile Ile Asn Leu Val Met Asn Ala Arg Asp Ala Met Glu Gly Arg Ser
610 615 620

Gly Glu Ile Lys Ile Arg Thr Trp Asn Gln Arg Val Glu Arg Gly Glu
625 630 635 640

Gly Arg Lys Gln Asp Met Val Val Leu Glu Val Ala Asp Ser Gly His
645 650 655

Gly Met Thr Thr Ala Val Lys Glu Gln Val Phe Glu Pro Phe Phe Thr
660 665 670

Thr Lys Gln Thr Gly Ser Gly Ser Gly Leu Gly Leu Ser Met Val Tyr
675 680 685

Gly Phe Val Arg Gln Ser Gly Gly Arg Val Gln Ile Glu Ser Glu Pro
690 695 700

Gly Lys Gly Thr Arg Val Cys Leu Gln Leu Pro Arg Ala Leu Thr Gln
705 710 715 720

Ser Leu Ile Glu Val Leu Pro Ala Leu Gly Ala Val Ala Asn Met Ala
725 730 735

Asp Gln Leu Val Leu Val Leu Glu Asp Glu Pro Asp Val Arg Gln Thr
740 745 750

Leu Cys Glu Gln Leu His Gln Leu Gly Tyr Leu Thr Leu Glu Thr Gly
755 760 765

Asp Ser Arg Gln Ala Leu Ala Leu Met Ala Asp Val Pro Asp Ile Ser
770 775 780

Ile Val Ile Ser Asp Leu Met Leu Pro Gly Asp Met Thr Gly Ala Glu

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785                 790                 795                 800

Val Leu Gln Gln Ala Arg Ser Val Tyr Pro His Leu Lys Leu Leu Leu
                805                 810                 815

Ile Ser Gly Gln Asp Leu Arg Arg Ser Lys Asn Phe Met Pro Glu Val
            820                 825                 830

Glu Leu Leu Arg Lys Pro Phe Asn Gln Gln Gln Leu Val Gln Ala Leu
        835                 840                 845

Gln Arg Val
    850



<210> 44
<211> 1764
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(1764)

<400> 44
atg gac gac tta acc ctg cgt tat ttt gac gct gaa atg cgc tac ctg      48
Met Asp Asp Leu Thr Leu Arg Tyr Phe Asp Ala Glu Met Arg Tyr Leu
1               5                   10                  15

cgc gaa gcg ggc gaa gag ttt gct cgt gcg cac cct gat cgg gct gcc      96
Arg Glu Ala Gly Glu Glu Phe Ala Arg Ala His Pro Asp Arg Ala Ala
            20                  25                  30

gga tta aat ctg gat aaa gcc ggg gcg cgt gac ccc tat gtc gaa cgc      144
Gly Leu Asn Leu Asp Lys Ala Gly Ala Arg Asp Pro Tyr Val Glu Arg
        35                  40                  45

cta ttt gaa ggc ttt gcc ttt ctg atg ggc cga ctg cgg gaa aaa ctg      192
Leu Phe Glu Gly Phe Ala Phe Leu Met Gly Arg Leu Arg Glu Lys Leu
    50                  55                  60

gat gac gac ctg ccg gaa ctg acc gaa ggg ttg gtc agc ctg ctg tgg      240
Asp Asp Asp Leu Pro Glu Leu Thr Glu Gly Leu Val Ser Leu Leu Trp
65                  70                  75                  80

ccg cac tac ctg cgt acc att ccg tcg ctt tct att gtg gag ttc acc      288
Pro His Tyr Leu Arg Thr Ile Pro Ser Leu Ser Ile Val Glu Phe Thr
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          85                   90                   95

cca caa tgg cag ggg atg aaa gag cgc atg ggg gtg agt aaa ggt ttt     336
Pro Gln Trp Gln Gly Met Lys Glu Arg Met Gly Val Ser Lys Gly Phe
            100                 105                 110

gaa gtg ctg tcc cgc ccc att ggt gaa cgt gaa acc cgt tgc cgc tat     384
Glu Val Leu Ser Arg Pro Ile Gly Glu Arg Glu Thr Arg Cys Arg Tyr
        115                 120                 125

acc acc acg caa gag atg gac ctg ctc ccg ctg acc ctg cgc cgt gcc     432
Thr Thr Thr Gln Glu Met Asp Leu Leu Pro Leu Thr Leu Arg Arg Ala
    130                 135                 140

ggg ctg gac agt gaa ccc gat ggc cgg tcg gtt atc cgg ctg cgc ttt     480
Gly Leu Asp Ser Glu Pro Asp Gly Arg Ser Val Ile Arg Leu Arg Phe
145                 150                 155                 160

gat tgc agc gcg ctg gcc gac tgg agc cgt atc aac ctg agc cgc ctg     528
Asp Cys Ser Ala Leu Ala Asp Trp Ser Arg Ile Asn Leu Ser Arg Leu
                165                 170                 175

ccg ctc tat ttt gat gcc gat gcg ccg ctg gcc tgc gcc ctg cat gag     576
Pro Leu Tyr Phe Asp Ala Asp Ala Pro Leu Ala Cys Ala Leu His Glu
            180                 185                 190

gcg ctg acc ctg aat acc gcc aaa ctc tgg atc cgt ttg ccg ggg cag     624
Ala Leu Thr Leu Asn Thr Ala Lys Leu Trp Ile Arg Leu Pro Gly Gln
        195                 200                 205

gct gat cgc cag ccg ctg gac ggc cat ttc gcg ccg ctg ggg ttc ggg     672
Ala Asp Arg Gln Pro Leu Asp Gly His Phe Ala Pro Leu Gly Phe Gly
    210                 215                 220

gag cag gat aca ctg tgg ccg aag gcc gac agt gcg ttc agt ggt tat     720
Glu Gln Asp Thr Leu Trp Pro Lys Ala Asp Ser Ala Phe Ser Gly Tyr
225                 230                 235                 240

cag ctc ttg ctg gag tac ttt acc ttc cgc gaa aag ttt atg ttt gtc     768
Gln Leu Leu Leu Glu Tyr Phe Thr Phe Arg Glu Lys Phe Met Phe Val
                245                 250                 255

gcg ttg cag ggg ctg gat ggg atc gag ctg ccg gcg gaa ctg ccg tgg     816
Ala Leu Gln Gly Leu Asp Gly Ile Glu Leu Pro Ala Glu Leu Pro Trp
            260                 265                 270

ttt gag att gat gtg gtg ctg gaa aaa cgc tgg caa cat gat ttc tcg     864
Phe Glu Ile Asp Val Val Leu Glu Lys Arg Trp Gln His Asp Phe Ser
```

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        275                 280                 285

ttc tcc gaa aag aac ctg cgc ctg cat tgt gtg ccg gtg att aac ctg     912
Phe Ser Glu Lys Asn Leu Arg Leu His Cys Val Pro Val Ile Asn Leu
    290                 295                 300

ttc ccg ctg gaa tcg gac ccg ctg tca ctt tct tca tta cag acc gaa     960
Phe Pro Leu Glu Ser Asp Pro Leu Ser Leu Ser Ser Leu Gln Thr Glu
305                 310                 315                 320

tac ctg ctg cgc cca atg cgc att cag gac ggt tat acc gaa gtg tat    1008
Tyr Leu Leu Arg Pro Met Arg Ile Gln Asp Gly Tyr Thr Glu Val Tyr
                325                 330                 335

tcg gtg gac tcg gtg atc tcc tcc cgt cat acc ggg cat cag gtc tat    1056
Ser Val Asp Ser Val Ile Ser Ser Arg His Thr Gly His Gln Val Tyr
            340                 345                 350

gtc cct ttc acc agc ttt cgc cac aag ggg ggg atg ttg cgc cat gat    1104
Val Pro Phe Thr Ser Phe Arg His Lys Gly Gly Met Leu Arg His Asp
        355                 360                 365

gcg ccg gag tat tac tac cat acg cgg gtc aaa cgc ggg cct tcg ggg    1152
Ala Pro Glu Tyr Tyr Tyr His Thr Arg Val Lys Arg Gly Pro Ser Gly
    370                 375                 380

tta cac gat acc tgg ctg gtg ctg ggg ggc gag gcg ttt gat aac cac    1200
Leu His Asp Thr Trp Leu Val Leu Gly Gly Glu Ala Phe Asp Asn His
385                 390                 395                 400

agc gta ccg gat aat gaa aat ttg tcg ctg agc ctg acc ggc acc aac    1248
Ser Val Pro Asp Asn Glu Asn Leu Ser Leu Ser Leu Thr Gly Thr Asn
                405                 410                 415

ggg cag tta ccg cgt aaa gcg ctg caa agc acg gtg ctg gat acg gcg    1296
Gly Gln Leu Pro Arg Lys Ala Leu Gln Ser Thr Val Leu Asp Thr Ala
            420                 425                 430

gtg aaa tcc acc ggg gct cag gtg cgg gtg cgt aat ctc tcc gcg ccg    1344
Val Lys Ser Thr Gly Ala Gln Val Arg Val Arg Asn Leu Ser Ala Pro
        435                 440                 445

tca ttg cca tgc tac ccg ccg aac cgc gac cgt ttt cac tgg cgg gtg    1392
Ser Leu Pro Cys Tyr Pro Pro Asn Arg Asp Arg Phe His Trp Arg Val
    450                 455                 460

ctg agc cat ctg ggc agt agt ttt ctg tgg atg atg gat aac gcc gaa    1440
Leu Ser His Leu Gly Ser Ser Phe Leu Trp Met Met Asp Asn Ala Glu
```

465 470 475 480

gtg ctg cgc ggc acg ctg gcg ctg tat gac tgg acg gac aac gaa atg 1488

Val Leu Arg Gly Thr Leu Ala Leu Tyr Asp Trp Thr Asp Asn Glu Met

485 490 495

aac cgc cgt cgg ctg gag gcg atc gcc gag gtc aaa cac agc gag att 1536

Asn Arg Arg Arg Leu Glu Ala Ile Ala Glu Val Lys His Ser Glu Ile

500 505 510

gaa cgc ttt gag cgg ggc tat ttg ctg cgc ggg gtg cac att gaa atc 1584

Glu Arg Phe Glu Arg Gly Tyr Leu Leu Arg Gly Val His Ile Glu Ile

515 520 525

acc ctc gac agc aac ggc ttt acc ggt acc ggg gat att tgt ctg ttt 1632

Thr Leu Asp Ser Asn Gly Phe Thr Gly Thr Gly Asp Ile Cys Leu Phe

530 535 540

ggg gaa atg ctc agt cgc ttc ttt gcc ctg tat acc gat att cac ctg 1680

Gly Glu Met Leu Ser Arg Phe Phe Ala Leu Tyr Thr Asp Ile His Leu

545 550 555 560

ttt aat cgt ctg act ctg ata ctg caa ccg aca gga gaa cgt ttg gaa 1728

Phe Asn Arg Leu Thr Leu Ile Leu Gln Pro Thr Gly Glu Arg Leu Glu

565 570 575

tgg gaa gag aat cat cag tcc cgc ctt ccc ggc taa 1764

Trp Glu Glu Asn His Gln Ser Arg Leu Pro Gly

580 585

<210> 45

<211> 587

<212> PRT

<213> Yersinia pestis

<400> 45

Met Asp Asp Leu Thr Leu Arg Tyr Phe Asp Ala Glu Met Arg Tyr Leu

1 5 10 15

Arg Glu Ala Gly Glu Glu Phe Ala Arg Ala His Pro Asp Arg Ala Ala

20 25 30

Gly Leu Asn Leu Asp Lys Ala Gly Ala Arg Asp Pro Tyr Val Glu Arg

35 40 45

Leu Phe Glu Gly Phe Ala Phe Leu Met Gly Arg Leu Arg Glu Lys Leu

50 55 60

```
Asp Asp Asp Leu Pro Glu Leu Thr Glu Gly Leu Val Ser Leu Leu Trp
65                  70                  75                  80

Pro His Tyr Leu Arg Thr Ile Pro Ser Leu Ser Ile Val Glu Phe Thr
                85                  90                  95

Pro Gln Trp Gln Gly Met Lys Glu Arg Met Gly Val Ser Lys Gly Phe
            100                 105                 110

Glu Val Leu Ser Arg Pro Ile Gly Glu Arg Glu Thr Arg Cys Arg Tyr
        115                 120                 125

Thr Thr Thr Gln Glu Met Asp Leu Leu Pro Leu Thr Leu Arg Arg Ala
    130                 135                 140

Gly Leu Asp Ser Glu Pro Asp Gly Arg Ser Val Ile Arg Leu Arg Phe
145                 150                 155                 160

Asp Cys Ser Ala Leu Ala Asp Trp Ser Arg Ile Asn Leu Ser Arg Leu
                165                 170                 175

Pro Leu Tyr Phe Asp Ala Asp Ala Pro Leu Ala Cys Ala Leu His Glu
            180                 185                 190

Ala Leu Thr Leu Asn Thr Ala Lys Leu Trp Ile Arg Leu Pro Gly Gln
        195                 200                 205

Ala Asp Arg Gln Pro Leu Asp Gly His Phe Ala Pro Leu Gly Phe Gly
    210                 215                 220

Glu Gln Asp Thr Leu Trp Pro Lys Ala Asp Ser Ala Phe Ser Gly Tyr
225                 230                 235                 240

Gln Leu Leu Leu Glu Tyr Phe Thr Phe Arg Glu Lys Phe Met Phe Val
                245                 250                 255

Ala Leu Gln Gly Leu Asp Gly Ile Glu Leu Pro Ala Glu Leu Pro Trp
            260                 265                 270

Phe Glu Ile Asp Val Val Leu Glu Lys Arg Trp Gln His Asp Phe Ser
        275                 280                 285

Phe Ser Glu Lys Asn Leu Arg Leu His Cys Val Pro Val Ile Asn Leu
    290                 295                 300

Phe Pro Leu Glu Ser Asp Pro Leu Ser Leu Ser Ser Leu Gln Thr Glu
305                 310                 315                 320
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```
Tyr Leu Leu Arg Pro Met Arg Ile Gln Asp Gly Tyr Thr Glu Val Tyr
                325                 330                 335

Ser Val Asp Ser Val Ile Ser Ser Arg His Thr Gly His Gln Val Tyr
            340                 345                 350

Val Pro Phe Thr Ser Phe Arg His Lys Gly Gly Met Leu Arg His Asp
        355                 360                 365

Ala Pro Glu Tyr Tyr Tyr His Thr Arg Val Lys Arg Gly Pro Ser Gly
    370                 375                 380

Leu His Asp Thr Trp Leu Val Leu Gly Gly Glu Ala Phe Asp Asn His
385                 390                 395                 400

Ser Val Pro Asp Asn Glu Asn Leu Ser Leu Ser Leu Thr Gly Thr Asn
                405                 410                 415

Gly Gln Leu Pro Arg Lys Ala Leu Gln Ser Thr Val Leu Asp Thr Ala
            420                 425                 430

Val Lys Ser Thr Gly Ala Gln Val Arg Val Arg Asn Leu Ser Ala Pro
        435                 440                 445

Ser Leu Pro Cys Tyr Pro Pro Asn Arg Asp Arg Phe His Trp Arg Val
    450                 455                 460

Leu Ser His Leu Gly Ser Ser Phe Leu Trp Met Met Asp Asn Ala Glu
465                 470                 475                 480

Val Leu Arg Gly Thr Leu Ala Leu Tyr Asp Trp Thr Asp Asn Glu Met
                485                 490                 495

Asn Arg Arg Arg Leu Glu Ala Ile Ala Glu Val Lys His Ser Glu Ile
            500                 505                 510

Glu Arg Phe Glu Arg Gly Tyr Leu Leu Arg Gly Val His Ile Glu Ile
        515                 520                 525

Thr Leu Asp Ser Asn Gly Phe Thr Gly Thr Gly Asp Ile Cys Leu Phe
    530                 535                 540

Gly Glu Met Leu Ser Arg Phe Phe Ala Leu Tyr Thr Asp Ile His Leu
545                 550                 555                 560

Phe Asn Arg Leu Thr Leu Ile Leu Gln Pro Thr Gly Glu Arg Leu Glu
                565                 570                 575
```

```
Trp Glu Glu Asn His Gln Ser Arg Leu Pro Gly
            580                 585



<210> 46
<211> 669
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(669)

<400> 46
atg ttg tca ggt att caa tcg gca tca cta ata tgt cat tcg tct tca      48
Met Leu Ser Gly Ile Gln Ser Ala Ser Leu Ile Cys His Ser Ser Ser
1               5                   10                  15

ata gaa gaa agt gaa aaa att caa tca gtt gtt ttt tta tct gat atc      96
Ile Glu Glu Ser Glu Lys Ile Gln Ser Val Val Phe Leu Ser Asp Ile
            20                  25                  30

ggt ctt gat aaa aac agg tta aca cta gag caa gaa aag gga ttg aag     144
Gly Leu Asp Lys Asn Arg Leu Thr Leu Glu Gln Glu Lys Gly Leu Lys
        35                  40                  45

gat ata aaa tca tct ata gat gat tgt tat cac aac ggt att agt act     192
Asp Ile Lys Ser Ser Ile Asp Asp Cys Tyr His Asn Gly Ile Ser Thr
    50                  55                  60

agt act ggc agg aaa aaa ata aaa gaa tta aga aat aaa gtt acc cag     240
Ser Thr Gly Arg Lys Lys Ile Lys Glu Leu Arg Asn Lys Val Thr Gln
65                  70                  75                  80

tac att aac tct gta gag agt tac cgg gat aag att tat gat gtt atc     288
Tyr Ile Asn Ser Val Glu Ser Tyr Arg Asp Lys Ile Tyr Asp Val Ile
                85                  90                  95

att gat aaa aga acg ggc aga ggt gaa aag ata ata tta aaa tct gga     336
Ile Asp Lys Arg Thr Gly Arg Gly Glu Lys Ile Ile Leu Lys Ser Gly
            100                 105                 110

tgt gat gaa aca cat aga aat agt tat ctt aag ggg att att tat ctc     384
Cys Asp Glu Thr His Arg Asn Ser Tyr Leu Lys Gly Ile Ile Tyr Leu
        115                 120                 125
```

```
agt aaa ttg cag gat ctt att cgt aat gaa ata gat aat gca cct att      432
Ser Lys Leu Gln Asp Leu Ile Arg Asn Glu Ile Asp Asn Ala Pro Ile
    130                 135                 140

aaa tat aaa aaa tca cta agt aaa gtt ttt gat gtc atg gga aaa ggc      480
Lys Tyr Lys Lys Ser Leu Ser Lys Val Phe Asp Val Met Gly Lys Gly
145                 150                 155                 160

gct gtg tat ggc gac ata aag gca ctg aat gaa gat cgt aaa ttg cct      528
Ala Val Tyr Gly Asp Ile Lys Ala Leu Asn Glu Asp Arg Lys Leu Pro
                165                 170                 175

gat ttt aaa tat agt gac tct gaa tgt tct gcg tat gat tat agc tat      576
Asp Phe Lys Tyr Ser Asp Ser Glu Cys Ser Ala Tyr Asp Tyr Ser Tyr
            180                 185                 190

ggt aac cat gca ctt gaa tgt ggt att cgc tct ttg gaa tgc gca gga      624
Gly Asn His Ala Leu Glu Cys Gly Ile Arg Ser Leu Glu Cys Ala Gly
        195                 200                 205

cag act gga tta ctg atc tgt atg tgt cta atg gga ggg aaa tga          669
Gln Thr Gly Leu Leu Ile Cys Met Cys Leu Met Gly Gly Lys
    210                 215                 220


<210> 47
<211> 222
<212> PRT
<213> Yersinia pestis

<400> 47
Met Leu Ser Gly Ile Gln Ser Ala Ser Leu Ile Cys His Ser Ser Ser
1               5                   10                  15

Ile Glu Glu Ser Glu Lys Ile Gln Ser Val Val Phe Leu Ser Asp Ile
            20                  25                  30

Gly Leu Asp Lys Asn Arg Leu Thr Leu Glu Gln Glu Lys Gly Leu Lys
        35                  40                  45

Asp Ile Lys Ser Ser Ile Asp Asp Cys Tyr His Asn Gly Ile Ser Thr
    50                  55                  60

Ser Thr Gly Arg Lys Lys Ile Lys Glu Leu Arg Asn Lys Val Thr Gln
65                  70                  75                  80

Tyr Ile Asn Ser Val Glu Ser Tyr Arg Asp Lys Ile Tyr Asp Val Ile
                85                  90                  95
```

```
Ile Asp Lys Arg Thr Gly Arg Gly Glu Lys Ile Ile Leu Lys Ser Gly
            100                 105                 110

Cys Asp Glu Thr His Arg Asn Ser Tyr Leu Lys Gly Ile Ile Tyr Leu
        115                 120                 125

Ser Lys Leu Gln Asp Leu Ile Arg Asn Glu Ile Asp Asn Ala Pro Ile
    130                 135                 140

Lys Tyr Lys Lys Ser Leu Ser Lys Val Phe Asp Val Met Gly Lys Gly
145                 150                 155                 160

Ala Val Tyr Gly Asp Ile Lys Ala Leu Asn Glu Asp Arg Lys Leu Pro
                165                 170                 175

Asp Phe Lys Tyr Ser Asp Ser Glu Cys Ser Ala Tyr Asp Tyr Ser Tyr
            180                 185                 190

Gly Asn His Ala Leu Glu Cys Gly Ile Arg Ser Leu Glu Cys Ala Gly
        195                 200                 205

Gln Thr Gly Leu Leu Ile Cys Met Cys Leu Met Gly Gly Lys
    210                 215                 220



<210> 48
<211> 1602
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(1602)

<400> 48
atg gcg acg tta act acc ttg ctc acc gct tgt gcc gca gag cct gag      48
Met Ala Thr Leu Thr Thr Leu Leu Thr Ala Cys Ala Ala Glu Pro Glu
 1              5                   10                  15

cca ctt tta cag cag gcc aga caa cag gtt gcg ctc tgg gaa cgt tgg      96
Pro Leu Leu Gln Gln Ala Arg Gln Gln Val Ala Leu Trp Glu Arg Trp
            20                  25                  30

ttg caa ccg gtg aca ccc gat aag cat acc ggt gaa gac ccc ggt tac     144
Leu Gln Pro Val Thr Pro Asp Lys His Thr Gly Glu Asp Pro Gly Tyr
        35                  40                  45
```

```
gat gac cac ttc caa cag atg cgt gaa gag gtc aat aag ctc tcg ggt     192
Asp Asp His Phe Gln Gln Met Arg Glu Glu Val Asn Lys Leu Ser Gly
     50                  55                  60

gcc gat acc acg ctg acc tgc gag ctg gct gaa aag ctg ttc acc aca     240
Ala Asp Thr Thr Leu Thr Cys Glu Leu Ala Glu Lys Leu Phe Thr Thr
 65                  70                  75                  80

cac ggc aag gat gtg cgg gtg gca acc tat tac gtc tgg gcg cgg ttg     288
His Gly Lys Asp Val Arg Val Ala Thr Tyr Tyr Val Trp Ala Arg Leu
                 85                  90                  95

cac cgt gac ggc gag gcc ggg ctg gcg gat ggc ctt tcc ctg ctg gcc     336
His Arg Asp Gly Glu Ala Gly Leu Ala Asp Gly Leu Ser Leu Leu Ala
            100                 105                 110

ggg ctg atc acg cgc ttt ggt gag ggc ctg cat ccg ctg cgt aca acc     384
Gly Leu Ile Thr Arg Phe Gly Glu Gly Leu His Pro Leu Arg Thr Thr
        115                 120                 125

agc cgg aaa acc gcg ttg gag tgg ctg gcc ggc tcc cgg atg cgc gac     432
Ser Arg Lys Thr Ala Leu Glu Trp Leu Ala Gly Ser Arg Met Arg Asp
    130                 135                 140

agc ttg tca ctt tac ccg gaa gtg gat aaa gcc gat ttt gag cgt atc     480
Ser Leu Ser Leu Tyr Pro Glu Val Asp Lys Ala Asp Phe Glu Arg Ile
145                 150                 155                 160

gtg ggc gca ctg gcc ctt atc gaa cag agg ctc agt ctc tgg gac gaa     528
Val Gly Ala Leu Ala Leu Ile Glu Gln Arg Leu Ser Leu Trp Asp Glu
                165                 170                 175

ggc gtc cgg ccg caa ctg ggc ggg ttg tat acc gcc ctg gaa aac cgc     576
Gly Val Arg Pro Gln Leu Gly Gly Leu Tyr Thr Ala Leu Glu Asn Arg
            180                 185                 190

ctc gcg caa tct ggt ggg cta aat gcc gtg gtg ccg caa aac agc agc     624
Leu Ala Gln Ser Gly Gly Leu Asn Ala Val Val Pro Gln Asn Ser Ser
        195                 200                 205

ggg tca tca tcg gca ggc agc ttg aac cca gcc aac acg gcg tca ccg     672
Gly Ser Ser Ser Ala Gly Ser Leu Asn Pro Ala Asn Thr Ala Ser Pro
    210                 215                 220

gcg ttg cgg cca gtg caa tcg gga cgt gac ctg ctc gat cag acc aaa     720
Ala Leu Arg Pro Val Gln Ser Gly Arg Asp Leu Leu Asp Gln Thr Lys
225                 230                 235                 240
```

```
acg ctg gca aaa tac ctg cgc aac cag ccg cag ggc tgg ctc tcc ggg      768
Thr Leu Ala Lys Tyr Leu Arg Asn Gln Pro Gln Gly Trp Leu Ser Gly
                245                 250                 255

cat cat ctt atc aaa agc gtg cgc tgg gat acg gta cat cag tca ccg      816
His His Leu Ile Lys Ser Val Arg Trp Asp Thr Val His Gln Ser Pro
            260                 265                 270

cca tta gat gtg aac gga cgg acc cgg ctg gta ccg ccg cgc ccg gaa      864
Pro Leu Asp Val Asn Gly Arg Thr Arg Leu Val Pro Pro Arg Pro Glu
        275                 280                 285

tat cgc gta caa ctc aag cgc ctt tat ctg caa caa aac tgg ctg gcg      912
Tyr Arg Val Gln Leu Lys Arg Leu Tyr Leu Gln Gln Asn Trp Leu Ala
    290                 295                 300

ttg ctg gaa cag gcc gaa tcg ata ttt gcc gaa ggg gtt aac cat ttc      960
Leu Leu Glu Gln Ala Glu Ser Ile Phe Ala Glu Gly Val Asn His Phe
305                 310                 315                 320

tgg ctc gat gtg cag tgg tat ctg cat cag gcc ctc agc aaa gcg ggg     1008
Trp Leu Asp Val Gln Trp Tyr Leu His Gln Ala Leu Ser Lys Ala Gly
                325                 330                 335

gcc cca ttc gat ggc tgg gcg agc tgt atc acg cag gat tta cgg tta     1056
Ala Pro Phe Asp Gly Trp Ala Ser Cys Ile Thr Gln Asp Leu Arg Leu
            340                 345                 350

tta ctg acc cgg ctg ccg ggg ctg gaa ggg cta tgc tgg agt gac ggc     1104
Leu Leu Thr Arg Leu Pro Gly Leu Glu Gly Leu Cys Trp Ser Asp Gly
        355                 360                 365

acg cca ttt gcc gat gag gtg acg ctg ggg tgg ata aac cag cag gta     1152
Thr Pro Phe Ala Asp Glu Val Thr Leu Gly Trp Ile Asn Gln Gln Val
    370                 375                 380

ctg gag tcg gtc tcg ggc tgg ggc agc gag ccg gcc gcc gtt tca tcc     1200
Leu Glu Ser Val Ser Gly Trp Gly Ser Glu Pro Ala Ala Val Ser Ser
385                 390                 395                 400

ggt gag gat ggc att ctg ttg ctg gag cca gaa gct ttg gct cag gcg     1248
Gly Glu Asp Gly Ile Leu Leu Leu Glu Pro Glu Ala Leu Ala Gln Ala
                405                 410                 415

gac agc gaa gga att gaa gcg gcg ctt aac tgg ttg cag tca cga ccg     1296
Asp Ser Glu Gly Ile Glu Ala Ala Leu Asn Trp Leu Gln Ser Arg Pro
            420                 425                 430
```

```
ggg atc acc acg gcg cgc cat cag tgg ctg ctg cgt ctg gtg atg gcc     1344
Gly Ile Thr Thr Ala Arg His Gln Trp Leu Leu Arg Leu Val Met Ala
        435                 440                 445

cgg gtg gcg gag cag tac ggt aag aac gat atg gcc ttg cat ctg ctg     1392
Arg Val Ala Glu Gln Tyr Gly Lys Asn Asp Met Ala Leu His Leu Leu
    450                 455                 460

agt ggc ctt gat agc agc ggc gcg ttg ttg acc ttg cca cag tgg gag     1440
Ser Gly Leu Asp Ser Ser Gly Ala Leu Leu Thr Leu Pro Gln Trp Glu
465                 470                 475                 480

ccg ggg ttg gtg ttt gaa gtt aaa gcc cgc cgt ttg aag ctg ttg cgt     1488
Pro Gly Leu Val Phe Glu Val Lys Ala Arg Arg Leu Lys Leu Leu Arg
                485                 490                 495

atg aag gca cag cgg ggt gac agt gat aaa acc cgc ctg cat gct gaa     1536
Met Lys Ala Gln Arg Gly Asp Ser Asp Lys Thr Arg Leu His Ala Glu
            500                 505                 510

atg gaa agc ctg ctc agt ggg ctt atc gcc ctc gac ccg gcc cgt gcg     1584
Met Glu Ser Leu Leu Ser Gly Leu Ile Ala Leu Asp Pro Ala Arg Ala
        515                 520                 525

gcc gta tta tgc gga taa                                             1602
Ala Val Leu Cys Gly
    530


<210> 49
<211> 533
<212> PRT
<213> Yersinia pestis

<400> 49
Met Ala Thr Leu Thr Thr Leu Leu Thr Ala Cys Ala Ala Glu Pro Glu
1               5                   10                  15

Pro Leu Leu Gln Gln Ala Arg Gln Gln Val Ala Leu Trp Glu Arg Trp
            20                  25                  30

Leu Gln Pro Val Thr Pro Asp Lys His Thr Gly Glu Asp Pro Gly Tyr
        35                  40                  45

Asp Asp His Phe Gln Gln Met Arg Glu Glu Val Asn Lys Leu Ser Gly
    50                  55                  60
```

```
Ala Asp Thr Thr Leu Thr Cys Glu Leu Ala Glu Lys Leu Phe Thr Thr
65                  70                  75                  80

His Gly Lys Asp Val Arg Val Ala Thr Tyr Tyr Val Trp Ala Arg Leu
                85                  90                  95

His Arg Asp Gly Glu Ala Gly Leu Ala Asp Gly Leu Ser Leu Leu Ala
            100                 105                 110

Gly Leu Ile Thr Arg Phe Gly Glu Gly Leu His Pro Leu Arg Thr Thr
        115                 120                 125

Ser Arg Lys Thr Ala Leu Glu Trp Leu Ala Gly Ser Arg Met Arg Asp
    130                 135                 140

Ser Leu Ser Leu Tyr Pro Glu Val Asp Lys Ala Asp Phe Glu Arg Ile
145                 150                 155                 160

Val Gly Ala Leu Ala Leu Ile Glu Gln Arg Leu Ser Leu Trp Asp Glu
                165                 170                 175

Gly Val Arg Pro Gln Leu Gly Gly Leu Tyr Thr Ala Leu Glu Asn Arg
            180                 185                 190

Leu Ala Gln Ser Gly Gly Leu Asn Ala Val Val Pro Gln Asn Ser Ser
        195                 200                 205

Gly Ser Ser Ser Ala Gly Ser Leu Asn Pro Ala Asn Thr Ala Ser Pro
    210                 215                 220

Ala Leu Arg Pro Val Gln Ser Gly Arg Asp Leu Leu Asp Gln Thr Lys
225                 230                 235                 240

Thr Leu Ala Lys Tyr Leu Arg Asn Gln Pro Gln Gly Trp Leu Ser Gly
                245                 250                 255

His His Leu Ile Lys Ser Val Arg Trp Asp Thr Val His Gln Ser Pro
            260                 265                 270

Pro Leu Asp Val Asn Gly Arg Thr Arg Leu Val Pro Pro Arg Pro Glu
        275                 280                 285

Tyr Arg Val Gln Leu Lys Arg Leu Tyr Leu Gln Gln Asn Trp Leu Ala
    290                 295                 300

Leu Leu Glu Gln Ala Glu Ser Ile Phe Ala Glu Gly Val Asn His Phe
305                 310                 315                 320
```

```
Trp Leu Asp Val Gln Trp Tyr Leu His Gln Ala Leu Ser Lys Ala Gly
                325                 330                 335

Ala Pro Phe Asp Gly Trp Ala Ser Cys Ile Thr Gln Asp Leu Arg Leu
            340                 345                 350

Leu Leu Thr Arg Leu Pro Gly Leu Glu Gly Leu Cys Trp Ser Asp Gly
        355                 360                 365

Thr Pro Phe Ala Asp Glu Val Thr Leu Gly Trp Ile Asn Gln Gln Val
    370                 375                 380

Leu Glu Ser Val Ser Gly Trp Gly Ser Glu Pro Ala Ala Val Ser Ser
385                 390                 395                 400

Gly Glu Asp Gly Ile Leu Leu Leu Glu Pro Glu Ala Leu Ala Gln Ala
                405                 410                 415

Asp Ser Glu Gly Ile Glu Ala Ala Leu Asn Trp Leu Gln Ser Arg Pro
            420                 425                 430

Gly Ile Thr Thr Ala Arg His Gln Trp Leu Leu Arg Leu Val Met Ala
        435                 440                 445

Arg Val Ala Glu Gln Tyr Gly Lys Asn Asp Met Ala Leu His Leu Leu
    450                 455                 460

Ser Gly Leu Asp Ser Ser Gly Ala Leu Leu Thr Leu Pro Gln Trp Glu
465                 470                 475                 480

Pro Gly Leu Val Phe Glu Val Lys Ala Arg Arg Leu Lys Leu Leu Arg
                485                 490                 495

Met Lys Ala Gln Arg Gly Asp Ser Asp Lys Thr Arg Leu His Ala Glu
            500                 505                 510

Met Glu Ser Leu Leu Ser Gly Leu Ile Ala Leu Asp Pro Ala Arg Ala
        515                 520                 525

Ala Val Leu Cys Gly
    530
```

<210> 50
<211> 2448
<212> DNA
<213> Yersinia pestis

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<220>
<221> CDS
<222> (1)..(2448)

<400> 50
atg att atc aga ttc cgg cta ccg cca tta tcg gta ctg ata tat ggc      48
Met Ile Ile Arg Phe Arg Leu Pro Pro Leu Ser Val Leu Ile Tyr Gly
1               5                   10                  15

tca ata ttg tta ccg tca ctg ata ccc ttg act att tta gga ggg agc      96
Ser Ile Leu Leu Pro Ser Leu Ile Pro Leu Thr Ile Leu Gly Gly Ser
            20                  25                  30

ctc cct ccg ccc tcg aca tca aca acg atg cct gat act acg tta tat     144
Leu Pro Pro Pro Ser Thr Ser Thr Thr Met Pro Asp Thr Thr Leu Tyr
        35                  40                  45

ctt gaa ctc gtg gtc aat gac cgt aac ttt ggg agt act gta cct att     192
Leu Glu Leu Val Val Asn Asp Arg Asn Phe Gly Ser Thr Val Pro Ile
    50                  55                  60

agt tac cgc aac aac cgt tat tac ctt tct caa tca cag cta aga acg     240
Ser Tyr Arg Asn Asn Arg Tyr Tyr Leu Ser Gln Ser Gln Leu Arg Thr
65                  70                  75                  80

att ggg ctt cct ata tca gag cca ctg gca ccc gag att gcc att gat     288
Ile Gly Leu Pro Ile Ser Glu Pro Leu Ala Pro Glu Ile Ala Ile Asp
                85                  90                  95

aat atg gcg ggc gtg aac gtt aaa tat gat gga gag aac caa cgc cta     336
Asn Met Ala Gly Val Asn Val Lys Tyr Asp Gly Glu Asn Gln Arg Leu
            100                 105                 110

tta atc aat gtt ccc agc gag tgg cta cca aag caa caa atc gag gtt     384
Leu Ile Asn Val Pro Ser Glu Trp Leu Pro Lys Gln Gln Ile Glu Val
        115                 120                 125

acc gaa caa gat gat ttc aat ctt gcg caa agt agt ttg ggg gct tta     432
Thr Glu Gln Asp Asp Phe Asn Leu Ala Gln Ser Ser Leu Gly Ala Leu
    130                 135                 140

ttc aat tac gat atc tat gcc aca caa ggt tac ccg tac tca tct tta     480
Phe Asn Tyr Asp Ile Tyr Ala Thr Gln Gly Tyr Pro Tyr Ser Ser Leu
145                 150                 155                 160

act cat ttt tca gca tgg aca gaa cag cgc att ttt gat cgt ttt ggc     528
Thr His Phe Ser Ala Trp Thr Glu Gln Arg Ile Phe Asp Arg Phe Gly
```

```
                165                 170                 175

ttg ctc agt aat acc ggc gtt tat cgc acc cac ttc cca agt aat aac   576
Leu Leu Ser Asn Thr Gly Val Tyr Arg Thr His Phe Pro Ser Asn Asn
            180                 185                 190

aac aca gat gac gcg aaa ggc tat att cgt ttt gat acc cag tgg cag   624
Asn Thr Asp Asp Ala Lys Gly Tyr Ile Arg Phe Asp Thr Gln Trp Gln
        195                 200                 205

aag aat gac gaa gaa cat ctg ctg cgt tat agc aca ggt gac ctc att   672
Lys Asn Asp Glu Glu His Leu Leu Arg Tyr Ser Thr Gly Asp Leu Ile
    210                 215                 220

acc ggt gct ttg cca tgg agc agt gcg ata cgt ctt ggc ggc att cag   720
Thr Gly Ala Leu Pro Trp Ser Ser Ala Ile Arg Leu Gly Gly Ile Gln
225                 230                 235                 240

ata gca cgg cat ttt gct att cgg ccc gat ctc ata acc tac cca tta   768
Ile Ala Arg His Phe Ala Ile Arg Pro Asp Leu Ile Thr Tyr Pro Leu
                245                 250                 255

cca caa ttt tct ggt cag gcc gca gtc ccc agc acc gtt gat ctc tac   816
Pro Gln Phe Ser Gly Gln Ala Ala Val Pro Ser Thr Val Asp Leu Tyr
            260                 265                 270

att gat aac ttc agg aca caa tcg gcc aat atc aac cca ggc cct ttt   864
Ile Asp Asn Phe Arg Thr Gln Ser Ala Asn Ile Asn Pro Gly Pro Phe
        275                 280                 285

gtc atc aat aat gca ccg cga atc aat ggt gca ggc caa gcg act atc   912
Val Ile Asn Asn Ala Pro Arg Ile Asn Gly Ala Gly Gln Ala Thr Ile
    290                 295                 300

gtc aca acc gat gcc ctt ggc agg caa atc agc aca tct gta ccc ttt   960
Val Thr Thr Asp Ala Leu Gly Arg Gln Ile Ser Thr Ser Val Pro Phe
305                 310                 315                 320

tac gtt gcc agt aca ctg cta aaa ccc gga gtg tgg gat ttc agt ctc   1008
Tyr Val Ala Ser Thr Leu Leu Lys Pro Gly Val Trp Asp Phe Ser Leu
                325                 330                 335

tcg ggg ggt gcc cta cgt cgt aat tat gcg att cgc tca gca gat tac   1056
Ser Gly Gly Ala Leu Arg Arg Asn Tyr Ala Ile Arg Ser Ala Asp Tyr
            340                 345                 350

ggt gaa atg gtt gcc agt ggt gtc gtt cgt tac ggc aca aca cct tgg   1104
Gly Glu Met Val Ala Ser Gly Val Val Arg Tyr Gly Thr Thr Pro Trp
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355 360 365

ttg aca ctg gag ggc cgg gga gac atc gcc aaa gaa atg cat gta att 1152
Leu Thr Leu Glu Gly Arg Gly Asp Ile Ala Lys Glu Met His Val Ile
370 375 380

ggg ggt ggc gtt aat ttt cgc atg ggg tta ttg ggt gtc cta aat agt 1200
Gly Gly Gly Val Asn Phe Arg Met Gly Leu Leu Gly Val Leu Asn Ser
385 390 395 400

gca tac agt ata agc aac aca tcg aac ggc gct ttt aac aat gtg gct 1248
Ala Tyr Ser Ile Ser Asn Thr Ser Asn Gly Ala Phe Asn Asn Val Ala
405 410 415

gaa ccg cta aat acc aat aat gcc acg ccg aat aga tta ccg tcc cca 1296
Glu Pro Leu Asn Thr Asn Asn Ala Thr Pro Asn Arg Leu Pro Ser Pro
420 425 430

gca gcg tca cgc cgt gga cgt ggc aac cag cgt tca tta ggc tat agc 1344
Ala Ala Ser Arg Arg Gly Arg Gly Asn Gln Arg Ser Leu Gly Tyr Ser
435 440 445

tac agt aat gca ttc ttt aat tta aat gct caa cat att atc tct agt 1392
Tyr Ser Asn Ala Phe Phe Asn Leu Asn Ala Gln His Ile Ile Ser Ser
450 455 460

gat gaa tac agt gac ctt gcc aat tat aaa acg cct tct ctc tta agc 1440
Asp Glu Tyr Ser Asp Leu Ala Asn Tyr Lys Thr Pro Ser Leu Leu Ser
465 470 475 480

cga cgc atg act caa ctc acg gga agt ctc agc ctc ggt agt tac ggc 1488
Arg Arg Met Thr Gln Leu Thr Gly Ser Leu Ser Leu Gly Ser Tyr Gly
485 490 495

acc gtg gga tcg ggt tac ttt gat gtc agg gat gct ctt ggc gaa caa 1536
Thr Val Gly Ser Gly Tyr Phe Asp Val Arg Asp Ala Leu Gly Glu Gln
500 505 510

acc cgg ctc att aat atc agc tac agc acc tca ctg tta cgc aat agc 1584
Thr Arg Leu Ile Asn Ile Ser Tyr Ser Thr Ser Leu Leu Arg Asn Ser
515 520 525

aac ttt tat agc gca cta aac cgt gag ctg ggc cgt aaa ggt tac aat 1632
Asn Phe Tyr Ser Ala Leu Asn Arg Glu Leu Gly Arg Lys Gly Tyr Asn
530 535 540

gta caa ctg gtc tgg agc att ccg tta ggc ccg cgg gga tca agc agc 1680
Val Gln Leu Val Trp Ser Ile Pro Leu Gly Pro Arg Gly Ser Ser Ser

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545                 550                 555                 560

atc agt gca acc cgc aca aat gat aac caa tgg att caa caa ctg aat    1728
Ile Ser Ala Thr Arg Thr Asn Asp Asn Gln Trp Ile Gln Gln Leu Asn
                565                 570                 575

tat agc cgt tca gcg ccc tcg aat ggg gga ttg ggc tgg aac ctc gct    1776
Tyr Ser Arg Ser Ala Pro Ser Asn Gly Gly Leu Gly Trp Asn Leu Ala
            580                 585                 590

tat gcc aac agc acg aat aac aat aat caa tac caa cag gca gac att    1824
Tyr Ala Asn Ser Thr Asn Asn Asn Asn Gln Tyr Gln Gln Ala Asp Ile
        595                 600                 605

gtt tgg cgt act tca atg atg gag agt cgc atg ggc cta tat ggt aac    1872
Val Trp Arg Thr Ser Met Met Glu Ser Arg Met Gly Leu Tyr Gly Asn
    610                 615                 620

agt aat aac tac aac tat tgg ggg gga tta acc ggt tca tta gtg gtg    1920
Ser Asn Asn Tyr Asn Tyr Trp Gly Gly Leu Thr Gly Ser Leu Val Val
625                 630                 635                 640

atg aat agg agt gtc tat gcc agc aat atg att aac gat gct ttt gct    1968
Met Asn Arg Ser Val Tyr Ala Ser Asn Met Ile Asn Asp Ala Phe Ala
                645                 650                 655

ttg gta tcg acc aat ggt ttt agt aat att ccg gtt agt tac gaa aat    2016
Leu Val Ser Thr Asn Gly Phe Ser Asn Ile Pro Val Ser Tyr Glu Asn
            660                 665                 670

caa ctt att ggc aca act aat gcc aag ggt tat ttg ctg atc ccg aca    2064
Gln Leu Ile Gly Thr Thr Asn Ala Lys Gly Tyr Leu Leu Ile Pro Thr
        675                 680                 685

gtc gcc tca tat tat cag gca aaa ttc cag att gac cca atg aat tta    2112
Val Ala Ser Tyr Tyr Gln Ala Lys Phe Gln Ile Asp Pro Met Asn Leu
    690                 695                 700

ccg gca gat gtc atg cta ccc aat gtt gaa cgg cgg tta gcc att ggt    2160
Pro Ala Asp Val Met Leu Pro Asn Val Glu Arg Arg Leu Ala Ile Gly
705                 710                 715                 720

gaa cgc agt ggc tat tta att aat ttc ccc att aag cga att tcc gca    2208
Glu Arg Ser Gly Tyr Leu Ile Asn Phe Pro Ile Lys Arg Ile Ser Ala
                725                 730                 735

gtg aat att aga att aca gac gca tca ggc caa gac tta ccg aaa ggc    2256
Val Asn Ile Arg Ile Thr Asp Ala Ser Gly Gln Asp Leu Pro Lys Gly
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740 745 750

agt gca ata tat act acc ggt aac atc ccc ata agt tat gtc ggt tgg 2304
Ser Ala Ile Tyr Thr Thr Gly Asn Ile Pro Ile Ser Tyr Val Gly Trp
755 760 765

gat ggc atg gta tat atc gag caa gtg gca caa tta aat aac ctt agg 2352
Asp Gly Met Val Tyr Ile Glu Gln Val Ala Gln Leu Asn Asn Leu Arg
770 775 780

att ata cgt gcc gat aat ggc aca cag tgc tac agc cag ttc aaa cta 2400
Ile Ile Arg Ala Asp Asn Gly Thr Gln Cys Tyr Ser Gln Phe Lys Leu
785 790 795 800

aag acg acg gaa ggt ata cag gat gct ggc acc aca gta tgc cga tag 2448
Lys Thr Thr Glu Gly Ile Gln Asp Ala Gly Thr Thr Val Cys Arg
805 810 815

<210> 51
<211> 815
<212> PRT
<213> Yersinia pestis

<400> 51
Met Ile Ile Arg Phe Arg Leu Pro Pro Leu Ser Val Leu Ile Tyr Gly
1 5 10 15

Ser Ile Leu Leu Pro Ser Leu Ile Pro Leu Thr Ile Leu Gly Gly Ser
20 25 30

Leu Pro Pro Pro Ser Thr Ser Thr Thr Met Pro Asp Thr Thr Leu Tyr
35 40 45

Leu Glu Leu Val Val Asn Asp Arg Asn Phe Gly Ser Thr Val Pro Ile
50 55 60

Ser Tyr Arg Asn Asn Arg Tyr Tyr Leu Ser Gln Ser Gln Leu Arg Thr
65 70 75 80

Ile Gly Leu Pro Ile Ser Glu Pro Leu Ala Pro Glu Ile Ala Ile Asp
85 90 95

Asn Met Ala Gly Val Asn Val Lys Tyr Asp Gly Glu Asn Gln Arg Leu
100 105 110

Leu Ile Asn Val Pro Ser Glu Trp Leu Pro Lys Gln Gln Ile Glu Val
115 120 125

```
Thr Glu Gln Asp Asp Phe Asn Leu Ala Gln Ser Ser Leu Gly Ala Leu
    130                 135                 140

Phe Asn Tyr Asp Ile Tyr Ala Thr Gln Gly Tyr Pro Tyr Ser Ser Leu
145                 150                 155                 160

Thr His Phe Ser Ala Trp Thr Glu Gln Arg Ile Phe Asp Arg Phe Gly
                165                 170                 175

Leu Leu Ser Asn Thr Gly Val Tyr Arg Thr His Phe Pro Ser Asn Asn
            180                 185                 190

Asn Thr Asp Asp Ala Lys Gly Tyr Ile Arg Phe Asp Thr Gln Trp Gln
        195                 200                 205

Lys Asn Asp Glu Glu His Leu Leu Arg Tyr Ser Thr Gly Asp Leu Ile
    210                 215                 220

Thr Gly Ala Leu Pro Trp Ser Ser Ala Ile Arg Leu Gly Gly Ile Gln
225                 230                 235                 240

Ile Ala Arg His Phe Ala Ile Arg Pro Asp Leu Ile Thr Tyr Pro Leu
                245                 250                 255

Pro Gln Phe Ser Gly Gln Ala Ala Val Pro Ser Thr Val Asp Leu Tyr
            260                 265                 270

Ile Asp Asn Phe Arg Thr Gln Ser Ala Asn Ile Asn Pro Gly Pro Phe
        275                 280                 285

Val Ile Asn Asn Ala Pro Arg Ile Asn Gly Ala Gly Gln Ala Thr Ile
    290                 295                 300

Val Thr Thr Asp Ala Leu Gly Arg Gln Ile Ser Thr Ser Val Pro Phe
305                 310                 315                 320

Tyr Val Ala Ser Thr Leu Leu Lys Pro Gly Val Trp Asp Phe Ser Leu
                325                 330                 335

Ser Gly Gly Ala Leu Arg Arg Asn Tyr Ala Ile Arg Ser Ala Asp Tyr
            340                 345                 350

Gly Glu Met Val Ala Ser Gly Val Val Arg Tyr Gly Thr Thr Pro Trp
        355                 360                 365

Leu Thr Leu Glu Gly Arg Gly Asp Ile Ala Lys Glu Met His Val Ile
    370                 375                 380
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Gly Gly Gly Val Asn Phe Arg Met Gly Leu Leu Gly Val Leu Asn Ser
385                 390                 395                 400

Ala Tyr Ser Ile Ser Asn Thr Ser Asn Gly Ala Phe Asn Asn Val Ala
                405                 410                 415

Glu Pro Leu Asn Thr Asn Asn Ala Thr Pro Asn Arg Leu Pro Ser Pro
            420                 425                 430

Ala Ala Ser Arg Arg Gly Arg Gly Asn Gln Arg Ser Leu Gly Tyr Ser
        435                 440                 445

Tyr Ser Asn Ala Phe Phe Asn Leu Asn Ala Gln His Ile Ile Ser Ser
    450                 455                 460

Asp Glu Tyr Ser Asp Leu Ala Asn Tyr Lys Thr Pro Ser Leu Leu Ser
465                 470                 475                 480

Arg Arg Met Thr Gln Leu Thr Gly Ser Leu Ser Leu Gly Ser Tyr Gly
                485                 490                 495

Thr Val Gly Ser Gly Tyr Phe Asp Val Arg Asp Ala Leu Gly Glu Gln
            500                 505                 510

Thr Arg Leu Ile Asn Ile Ser Tyr Ser Thr Ser Leu Leu Arg Asn Ser
        515                 520                 525

Asn Phe Tyr Ser Ala Leu Asn Arg Glu Leu Gly Arg Lys Gly Tyr Asn
    530                 535                 540

Val Gln Leu Val Trp Ser Ile Pro Leu Gly Pro Arg Gly Ser Ser Ser
545                 550                 555                 560

Ile Ser Ala Thr Arg Thr Asn Asp Asn Gln Trp Ile Gln Gln Leu Asn
                565                 570                 575

Tyr Ser Arg Ser Ala Pro Ser Asn Gly Gly Leu Gly Trp Asn Leu Ala
            580                 585                 590

Tyr Ala Asn Ser Thr Asn Asn Asn Asn Gln Tyr Gln Gln Ala Asp Ile
        595                 600                 605

Val Trp Arg Thr Ser Met Met Glu Ser Arg Met Gly Leu Tyr Gly Asn
    610                 615                 620

Ser Asn Asn Tyr Asn Tyr Trp Gly Gly Leu Thr Gly Ser Leu Val Val
625                 630                 635                 640
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Met Asn Arg Ser Val Tyr Ala Ser Asn Met Ile Asn Asp Ala Phe Ala
                645                 650                 655

Leu Val Ser Thr Asn Gly Phe Ser Asn Ile Pro Val Ser Tyr Glu Asn
            660                 665                 670

Gln Leu Ile Gly Thr Thr Asn Ala Lys Gly Tyr Leu Leu Ile Pro Thr
        675                 680                 685

Val Ala Ser Tyr Tyr Gln Ala Lys Phe Gln Ile Asp Pro Met Asn Leu
    690                 695                 700

Pro Ala Asp Val Met Leu Pro Asn Val Glu Arg Arg Leu Ala Ile Gly
705                 710                 715                 720

Glu Arg Ser Gly Tyr Leu Ile Asn Phe Pro Ile Lys Arg Ile Ser Ala
                725                 730                 735

Val Asn Ile Arg Ile Thr Asp Ala Ser Gly Gln Asp Leu Pro Lys Gly
            740                 745                 750

Ser Ala Ile Tyr Thr Thr Gly Asn Ile Pro Ile Ser Tyr Val Gly Trp
        755                 760                 765

Asp Gly Met Val Tyr Ile Glu Gln Val Ala Gln Leu Asn Asn Leu Arg
    770                 775                 780

Ile Ile Arg Ala Asp Asn Gly Thr Gln Cys Tyr Ser Gln Phe Lys Leu
785                 790                 795                 800

Lys Thr Thr Glu Gly Ile Gln Asp Ala Gly Thr Thr Val Cys Arg
                805                 810                 815


<210> 52
<211> 1233
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(1233)

<400> 52
atg gaa ata gtt aat ttt att agt gct cag gat ata gtt gag att gaa      48
Met Glu Ile Val Asn Phe Ile Ser Ala Gln Asp Ile Val Glu Ile Glu
```

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1               5                   10                  15

ttt ctc tca aca gag aat gaa aaa aat aaa gag gca ttg aat tca gta     96
Phe Leu Ser Thr Glu Asn Glu Lys Asn Lys Glu Ala Leu Asn Ser Val
            20                  25                  30

aat aaa tgg gag aat gat gct cca ttt ggg gaa aac aga acc aat gct     144
Asn Lys Trp Glu Asn Asp Ala Pro Phe Gly Glu Asn Arg Thr Asn Ala
        35                  40                  45

gct aat gaa att cgt gat gtt ata gag aga aat gcg cct ata ctt agg     192
Ala Asn Glu Ile Arg Asp Val Ile Glu Arg Asn Ala Pro Ile Leu Arg
    50                  55                  60

cta tcg cgt ctg aat atc agt tct tta cct gat gtt tta ccg cat agt     240
Leu Ser Arg Leu Asn Ile Ser Ser Leu Pro Asp Val Leu Pro His Ser
65                  70                  75                  80

ctc atc gag att gaa att tat tat tgc gat gaa tta tct act ctc cct     288
Leu Ile Glu Ile Glu Ile Tyr Tyr Cys Asp Glu Leu Ser Thr Leu Pro
                85                  90                  95

gac agt ttt cct tcc gag ctt act aag cta aaa att agc cat tgc cct     336
Asp Ser Phe Pro Ser Glu Leu Thr Lys Leu Lys Ile Ser His Cys Pro
            100                 105                 110

gaa att tca tct tta tat aag aat gca cca aag cgt ttg act aaa tta     384
Glu Ile Ser Ser Leu Tyr Lys Asn Ala Pro Lys Arg Leu Thr Lys Leu
        115                 120                 125

gaa ata ata tct tgt ccg aaa att tca aat gct ata att cca ctg cct     432
Glu Ile Ile Ser Cys Pro Lys Ile Ser Asn Ala Ile Ile Pro Leu Pro
    130                 135                 140

gaa tca tta caa tat att aaa tta gat ata gac tcg aaa gag cgc ctt     480
Glu Ser Leu Gln Tyr Ile Lys Leu Asp Ile Asp Ser Lys Glu Arg Leu
145                 150                 155                 160

tct ctc tcg ttt gat aaa ttt cct aaa aat tta aga ggt att aat tta     528
Ser Leu Ser Phe Asp Lys Phe Pro Lys Asn Leu Arg Gly Ile Asn Leu
                165                 170                 175

agt gat agt ttt tta att gaa aaa agc aaa ttc aag gat aga gag atc     576
Ser Asp Ser Phe Leu Ile Glu Lys Ser Lys Phe Lys Asp Arg Glu Ile
            180                 185                 190

cga ttg aat gtt cta gtg cca tcc gta gct cta gag ttt aaa tta ggg     624
Arg Leu Asn Val Leu Val Pro Ser Val Ala Leu Glu Phe Lys Leu Gly
```

```
        195                 200                 205

gac att cta tat gga att gct cag tgt caa cat gag gtg atg cag caa    672
Asp Ile Leu Tyr Gly Ile Ala Gln Cys Gln His Glu Val Met Gln Gln
    210                 215                 220

cta att aat ttt aat gac ttt tct aac aaa gat att tgt tcg caa aca    720
Leu Ile Asn Phe Asn Asp Phe Ser Asn Lys Asp Ile Cys Ser Gln Thr
225                 230                 235                 240

aca att act gat gct gtt tgg gaa cat cgt aat tat ttt tcc cgt gat    768
Thr Ile Thr Asp Ala Val Trp Glu His Arg Asn Tyr Phe Ser Arg Asp
                245                 250                 255

aaa tat aga gac gat gcg aca atc aaa gaa atg tta aat gat gct gat    816
Lys Tyr Arg Asp Asp Ala Thr Ile Lys Glu Met Leu Asn Asp Ala Asp
            260                 265                 270

cgc gga att aaa ttc aaa gat ttc cta gaa aaa cat gaa aag tat aat    864
Arg Gly Ile Lys Phe Lys Asp Phe Leu Glu Lys His Glu Lys Tyr Asn
        275                 280                 285

att tta agt cgt tcg gga ata aaa tca tac cgt cct cat aaa aat gag    912
Ile Leu Ser Arg Ser Gly Ile Lys Ser Tyr Arg Pro His Lys Asn Glu
    290                 295                 300

gag gat ata tgt tta tca agg acc agt aag gct ggt ctt gaa ttt cag    960
Glu Asp Ile Cys Leu Ser Arg Thr Ser Lys Ala Gly Leu Glu Phe Gln
305                 310                 315                 320

atc atg gaa agg caa gag cgt gta ttt ttt tgt ata gat aat ttg aat    1008
Ile Met Glu Arg Gln Glu Arg Val Phe Phe Cys Ile Asp Asn Leu Asn
                325                 330                 335

aat tgt att cct gaa att gca caa aaa aaa cct gat tat ggt acc tat    1056
Asn Cys Ile Pro Glu Ile Ala Gln Lys Lys Pro Asp Tyr Gly Thr Tyr
            340                 345                 350

atc aca gcc tct gag ttg aga tgg ctt tac cgt cgt aaa gat cac cct    1104
Ile Thr Ala Ser Glu Leu Arg Trp Leu Tyr Arg Arg Lys Asp His Pro
        355                 360                 365

aat gta aaa aat aat gtt caa ttc tgc ttg gag gga gca ttt att tca    1152
Asn Val Lys Asn Asn Val Gln Phe Cys Leu Glu Gly Ala Phe Ile Ser
    370                 375                 380

caa gaa gag gta ttt tca ctg cct ggt tgg gaa act tat ttt cct aaa    1200
Gln Glu Glu Val Phe Ser Leu Pro Gly Trp Glu Thr Tyr Phe Pro Lys
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385 390 395 400

aga aaa agt aac ttc ata cct tcc tat gtt tga 1233
Arg Lys Ser Asn Phe Ile Pro Ser Tyr Val
405 410

<210> 53
<211> 410
<212> PRT
<213> Yersinia pestis

<400> 53
Met Glu Ile Val Asn Phe Ile Ser Ala Gln Asp Ile Val Glu Ile Glu
1 5 10 15

Phe Leu Ser Thr Glu Asn Glu Lys Asn Lys Glu Ala Leu Asn Ser Val
20 25 30

Asn Lys Trp Glu Asn Asp Ala Pro Phe Gly Glu Asn Arg Thr Asn Ala
35 40 45

Ala Asn Glu Ile Arg Asp Val Ile Glu Arg Asn Ala Pro Ile Leu Arg
50 55 60

Leu Ser Arg Leu Asn Ile Ser Ser Leu Pro Asp Val Leu Pro His Ser
65 70 75 80

Leu Ile Glu Ile Glu Ile Tyr Tyr Cys Asp Glu Leu Ser Thr Leu Pro
85 90 95

Asp Ser Phe Pro Ser Glu Leu Thr Lys Leu Lys Ile Ser His Cys Pro
100 105 110

Glu Ile Ser Ser Leu Tyr Lys Asn Ala Pro Lys Arg Leu Thr Lys Leu
115 120 125

Glu Ile Ile Ser Cys Pro Lys Ile Ser Asn Ala Ile Ile Pro Leu Pro
130 135 140

Glu Ser Leu Gln Tyr Ile Lys Leu Asp Ile Asp Ser Lys Glu Arg Leu
145 150 155 160

Ser Leu Ser Phe Asp Lys Phe Pro Lys Asn Leu Arg Gly Ile Asn Leu
165 170 175

Ser Asp Ser Phe Leu Ile Glu Lys Ser Lys Phe Lys Asp Arg Glu Ile
180 185 190

```
Arg Leu Asn Val Leu Val Pro Ser Val Ala Leu Glu Phe Lys Leu Gly
        195                 200                 205

Asp Ile Leu Tyr Gly Ile Ala Gln Cys Gln His Glu Val Met Gln Gln
    210                 215                 220

Leu Ile Asn Phe Asn Asp Phe Ser Asn Lys Asp Ile Cys Ser Gln Thr
225                 230                 235                 240

Thr Ile Thr Asp Ala Val Trp Glu His Arg Asn Tyr Phe Ser Arg Asp
                245                 250                 255

Lys Tyr Arg Asp Asp Ala Thr Ile Lys Glu Met Leu Asn Asp Ala Asp
            260                 265                 270

Arg Gly Ile Lys Phe Lys Asp Phe Leu Glu Lys His Glu Lys Tyr Asn
        275                 280                 285

Ile Leu Ser Arg Ser Gly Ile Lys Ser Tyr Arg Pro His Lys Asn Glu
    290                 295                 300

Glu Asp Ile Cys Leu Ser Arg Thr Ser Lys Ala Gly Leu Glu Phe Gln
305                 310                 315                 320

Ile Met Glu Arg Gln Glu Arg Val Phe Phe Cys Ile Asp Asn Leu Asn
                325                 330                 335

Asn Cys Ile Pro Glu Ile Ala Gln Lys Lys Pro Asp Tyr Gly Thr Tyr
            340                 345                 350

Ile Thr Ala Ser Glu Leu Arg Trp Leu Tyr Arg Arg Lys Asp His Pro
        355                 360                 365

Asn Val Lys Asn Asn Val Gln Phe Cys Leu Glu Gly Ala Phe Ile Ser
    370                 375                 380

Gln Glu Glu Val Phe Ser Leu Pro Gly Trp Glu Thr Tyr Phe Pro Lys
385                 390                 395                 400

Arg Lys Ser Asn Phe Ile Pro Ser Tyr Val
                405                 410
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<210> 54
<211> 2082
<212> DNA

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<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(2082)

<400> 54
atg aaa ggc cgc cta ctg gac gcc gta ccc ctc agt aca ctt tcc gga      48
Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Thr Leu Ser Gly
 1               5                  10                  15

gtt ggc gca agt cag gct gga aaa ctc gcc aag ata ggt ttg gaa acc      96
Val Gly Ala Ser Gln Ala Gly Lys Leu Ala Lys Ile Gly Leu Glu Thr
            20                  25                  30

att cag gac ctg ctg ctg cac ctt ccg cta cgt tat gag gat cgt act     144
Ile Gln Asp Leu Leu Leu His Leu Pro Leu Arg Tyr Glu Asp Arg Thr
        35                  40                  45

cgt cta tat cgt att ggt gat ctg ctg ccc ggt ctt tcg gtc acg gtt     192
Arg Leu Tyr Arg Ile Gly Asp Leu Leu Pro Gly Leu Ser Val Thr Val
    50                  55                  60

gaa ggt gaa gtt cta cgc tct gat att agc ttt ggt cgc cgc cgt atg     240
Glu Gly Glu Val Leu Arg Ser Asp Ile Ser Phe Gly Arg Arg Arg Met
65                  70                  75                  80

atg acc tgt caa atc agc gat ggt agc ggc gtt ctc acc ctg cgc ttt     288
Met Thr Cys Gln Ile Ser Asp Gly Ser Gly Val Leu Thr Leu Arg Phe
                85                  90                  95

ttt aac ttc aat gca gca atg aaa aac agt ctg tca gta ggc aaa cat     336
Phe Asn Phe Asn Ala Ala Met Lys Asn Ser Leu Ser Val Gly Lys His
            100                 105                 110

gtc att gct tat ggc gaa gcc aaa cga ggc aat aac ggg cca gaa atc     384
Val Ile Ala Tyr Gly Glu Ala Lys Arg Gly Asn Asn Gly Pro Glu Ile
        115                 120                 125

att cac cct gaa tat cgg gtt cat ggc gag aat att ggc gtt gaa tta     432
Ile His Pro Glu Tyr Arg Val His Gly Glu Asn Ile Gly Val Glu Leu
    130                 135                 140

cag gaa tcg ctg aca cca gtc tat ccc acg acc gag ggc att cgt cag     480
Gln Glu Ser Leu Thr Pro Val Tyr Pro Thr Thr Glu Gly Ile Arg Gln
145                 150                 155                 160

gca act ctg cgc aaa ctt atc gat cag gca ctg gca atg ctg gac acc     528
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```
Ala Thr Leu Arg Lys Leu Ile Asp Gln Ala Leu Ala Met Leu Asp Thr
                165                 170                 175

tgt gtt att gct gag tta ctg cca att gaa ttg agc cgt tct ctc atc    576
Cys Val Ile Ala Glu Leu Leu Pro Ile Glu Leu Ser Arg Ser Leu Ile
            180                 185                 190

agc ctg cct gaa gcg att cat act ctg cat cgc cct ccg gca gat att    624
Ser Leu Pro Glu Ala Ile His Thr Leu His Arg Pro Pro Ala Asp Ile
        195                 200                 205

caa tta gct gat tta gaa caa ggg aag cac ccc gct caa cgg cgt ctg    672
Gln Leu Ala Asp Leu Glu Gln Gly Lys His Pro Ala Gln Arg Arg Leu
    210                 215                 220

atc atg gaa gag ttg ctg gct cat aac ctc agt atg ttg gca gtc agg    720
Ile Met Glu Glu Leu Leu Ala His Asn Leu Ser Met Leu Ala Val Arg
225                 230                 235                 240

gcg ggt gca caa agc tac cga gca ttg cca tta atg gcc gaa gag cag    768
Ala Gly Ala Gln Ser Tyr Arg Ala Leu Pro Leu Met Ala Glu Glu Gln
                245                 250                 255

ctt aaa caa cgt ttt ctg gcc gcc cta cct ttt acg cct act caa gcc    816
Leu Lys Gln Arg Phe Leu Ala Ala Leu Pro Phe Thr Pro Thr Gln Ala
            260                 265                 270

cag caa cgg gtc gtc gcc gaa att gaa cgg gat atg acc caa agt ttc    864
Gln Gln Arg Val Val Ala Glu Ile Glu Arg Asp Met Thr Gln Ser Phe
        275                 280                 285

ccg atg atg cga ctg att cag ggg gat gta ggt tcc ggt aaa aca ctg    912
Pro Met Met Arg Leu Ile Gln Gly Asp Val Gly Ser Gly Lys Thr Leu
    290                 295                 300

gta gcc gca ctg gcc gcg cta cgg gcc atc gct cac ggt aag cag gtt    960
Val Ala Ala Leu Ala Ala Leu Arg Ala Ile Ala His Gly Lys Gln Val
305                 310                 315                 320

gcc ctg atg gca ccg acc gaa ctg ctg gca gaa cag cac gcc act act    1008
Ala Leu Met Ala Pro Thr Glu Leu Leu Ala Glu Gln His Ala Thr Thr
                325                 330                 335

ttc cgt caa tgg ctg gag cct ctt ggg ttt agt gtc ggc tgg ttg gct    1056
Phe Arg Gln Trp Leu Glu Pro Leu Gly Phe Ser Val Gly Trp Leu Ala
            340                 345                 350

ggc aag caa aag ggg aaa gcg cgg tta gca caa caa gag gcc gtt gcc    1104
```

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Gly Lys Gln Lys Gly Lys Ala Arg Leu Ala Gln Gln Glu Ala Val Ala
        355                 360                 365

agc ggt cag gtc tcc atg gtg atc ggt act cat gcc atg ttt caa gaa    1152
Ser Gly Gln Val Ser Met Val Ile Gly Thr His Ala Met Phe Gln Glu
    370                 375                 380

cag gtg caa ttc tcg ggg tta gca ctg gta att att gat gag cag cat    1200
Gln Val Gln Phe Ser Gly Leu Ala Leu Val Ile Ile Asp Glu Gln His
385                 390                 395                 400

cgt ttc ggt gtt cac cag cgc ctc acg tta tgg gaa aaa ggt gag gag    1248
Arg Phe Gly Val His Gln Arg Leu Thr Leu Trp Glu Lys Gly Glu Glu
                405                 410                 415

caa ggc ttc cat cca cat caa tta atc atg acg gca acc ccg atc cca    1296
Gln Gly Phe His Pro His Gln Leu Ile Met Thr Ala Thr Pro Ile Pro
            420                 425                 430

aga aca tta gcc atg act gcc tat gca gat ctc gat acc tcc gtg att    1344
Arg Thr Leu Ala Met Thr Ala Tyr Ala Asp Leu Asp Thr Ser Val Ile
        435                 440                 445

gat gaa tta ccg cca ggc aga acc ccc gtg aca acg gtg gca atc ccg    1392
Asp Glu Leu Pro Pro Gly Arg Thr Pro Val Thr Thr Val Ala Ile Pro
    450                 455                 460

gat act cgc cgt agt gat gtt att cag cgg gtt aaa aac gcg tgc ctg    1440
Asp Thr Arg Arg Ser Asp Val Ile Gln Arg Val Lys Asn Ala Cys Leu
465                 470                 475                 480

gaa gag ggt agg caa gca tat tgg gta tgt acc ttg att gaa gaa tca    1488
Glu Glu Gly Arg Gln Ala Tyr Trp Val Cys Thr Leu Ile Glu Glu Ser
                485                 490                 495

gag ttg ctg gag gct cag gct gca gag gta acg tgc gaa gag ctg aaa    1536
Glu Leu Leu Glu Ala Gln Ala Ala Glu Val Thr Cys Glu Glu Leu Lys
            500                 505                 510

att gcc tta ccg gaa att aaa gtt ggc ttg gtt cat ggg cgg atg aaa    1584
Ile Ala Leu Pro Glu Ile Lys Val Gly Leu Val His Gly Arg Met Lys
        515                 520                 525

ggc ccc gaa aaa cag gcg att atg ctg gcc ttt aaa caa ggt gag cta    1632
Gly Pro Glu Lys Gln Ala Ile Met Leu Ala Phe Lys Gln Gly Glu Leu
    530                 535                 540

cag tta ttg gtc gca acc acg gtg att gaa gtg gga gtt gat gtg ccc    1680
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Gln Leu Leu Val Ala Thr Thr Val Ile Glu Val Gly Val Asp Val Pro
545 550 555 560

aat gcc agc ttg atg att atc gat aat cct gaa cgg ttg ggg ctg gcg 1728
Asn Ala Ser Leu Met Ile Ile Asp Asn Pro Glu Arg Leu Gly Leu Ala
565 570 575

cag tta cat cag tta cgt ggg cgt gtc ggg cgc ggt gct gtc gct tcc 1776
Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
580 585 590

cac tgc gta tta ctc tat aaa acg cca tta agt aaa acc gct caa atg 1824
His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Met
595 600 605

cgg ttg cag gta tta cgt gat agc aat gat ggt ttt gtg att gca cag 1872
Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
610 615 620

cga gat cta gaa atc cgt ggc ccc ggt gag cta ttg ggc aca cgg caa 1920
Arg Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
625 630 635 640

aca ggt agc gca gag ttt aag gtt gcc gac cta ctt cgt gat caa gcg 1968
Thr Gly Ser Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
645 650 655

atg atc cca gaa gtt cag cgg gtc gcc cgt cat ctg cat caa cag tac 2016
Met Ile Pro Glu Val Gln Arg Val Ala Arg His Leu His Gln Gln Tyr
660 665 670

cct gaa cat gcc aag gca ttg ata gaa cgc tgg ttg ccg gag cgg gta 2064
Pro Glu His Ala Lys Ala Leu Ile Glu Arg Trp Leu Pro Glu Arg Val
675 680 685

cgg tat acc aat gcg taa 2082
Arg Tyr Thr Asn Ala
690

<210> 55
<211> 693
<212> PRT
<213> Yersinia pestis

<400> 55
Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Thr Leu Ser Gly
1 5 10 15

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Val Gly Ala Ser Gln Ala Gly Lys Leu Ala Lys Ile Gly Leu Glu Thr
            20                  25                  30

Ile Gln Asp Leu Leu Leu His Leu Pro Leu Arg Tyr Glu Asp Arg Thr
        35                  40                  45

Arg Leu Tyr Arg Ile Gly Asp Leu Leu Pro Gly Leu Ser Val Thr Val
    50                  55                  60

Glu Gly Glu Val Leu Arg Ser Asp Ile Ser Phe Gly Arg Arg Arg Met
65                  70                  75                  80

Met Thr Cys Gln Ile Ser Asp Gly Ser Gly Val Leu Thr Leu Arg Phe
                85                  90                  95

Phe Asn Phe Asn Ala Ala Met Lys Asn Ser Leu Ser Val Gly Lys His
            100                 105                 110

Val Ile Ala Tyr Gly Glu Ala Lys Arg Gly Asn Asn Gly Pro Glu Ile
        115                 120                 125

Ile His Pro Glu Tyr Arg Val His Gly Glu Asn Ile Gly Val Glu Leu
    130                 135                 140

Gln Glu Ser Leu Thr Pro Val Tyr Pro Thr Thr Glu Gly Ile Arg Gln
145                 150                 155                 160

Ala Thr Leu Arg Lys Leu Ile Asp Gln Ala Leu Ala Met Leu Asp Thr
                165                 170                 175

Cys Val Ile Ala Glu Leu Leu Pro Ile Glu Leu Ser Arg Ser Leu Ile
            180                 185                 190

Ser Leu Pro Glu Ala Ile His Thr Leu His Arg Pro Pro Ala Asp Ile
        195                 200                 205

Gln Leu Ala Asp Leu Glu Gln Gly Lys His Pro Ala Gln Arg Arg Leu
    210                 215                 220

Ile Met Glu Glu Leu Leu Ala His Asn Leu Ser Met Leu Ala Val Arg
225                 230                 235                 240

Ala Gly Ala Gln Ser Tyr Arg Ala Leu Pro Leu Met Ala Glu Glu Gln
                245                 250                 255

Leu Lys Gln Arg Phe Leu Ala Ala Leu Pro Phe Thr Pro Thr Gln Ala
            260                 265                 270
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Gln Gln Arg Val Val Ala Glu Ile Glu Arg Asp Met Thr Gln Ser Phe
        275                 280                 285

Pro Met Met Arg Leu Ile Gln Gly Asp Val Gly Ser Gly Lys Thr Leu
    290                 295                 300

Val Ala Ala Leu Ala Ala Leu Arg Ala Ile Ala His Gly Lys Gln Val
305                 310                 315                 320

Ala Leu Met Ala Pro Thr Glu Leu Leu Ala Glu Gln His Ala Thr Thr
                325                 330                 335

Phe Arg Gln Trp Leu Glu Pro Leu Gly Phe Ser Val Gly Trp Leu Ala
            340                 345                 350

Gly Lys Gln Lys Gly Lys Ala Arg Leu Ala Gln Gln Glu Ala Val Ala
        355                 360                 365

Ser Gly Gln Val Ser Met Val Ile Gly Thr His Ala Met Phe Gln Glu
    370                 375                 380

Gln Val Gln Phe Ser Gly Leu Ala Leu Val Ile Ile Asp Glu Gln His
385                 390                 395                 400

Arg Phe Gly Val His Gln Arg Leu Thr Leu Trp Glu Lys Gly Glu Glu
                405                 410                 415

Gln Gly Phe His Pro His Gln Leu Ile Met Thr Ala Thr Pro Ile Pro
            420                 425                 430

Arg Thr Leu Ala Met Thr Ala Tyr Ala Asp Leu Asp Thr Ser Val Ile
        435                 440                 445

Asp Glu Leu Pro Pro Gly Arg Thr Pro Val Thr Thr Val Ala Ile Pro
    450                 455                 460

Asp Thr Arg Arg Ser Asp Val Ile Gln Arg Val Lys Asn Ala Cys Leu
465                 470                 475                 480

Glu Glu Gly Arg Gln Ala Tyr Trp Val Cys Thr Leu Ile Glu Glu Ser
                485                 490                 495

Glu Leu Leu Glu Ala Gln Ala Ala Glu Val Thr Cys Glu Glu Leu Lys
            500                 505                 510

Ile Ala Leu Pro Glu Ile Lys Val Gly Leu Val His Gly Arg Met Lys
        515                 520                 525
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Gly Pro Glu Lys Gln Ala Ile Met Leu Ala Phe Lys Gln Gly Glu Leu
    530                 535                 540

Gln Leu Leu Val Ala Thr Thr Val Ile Glu Val Gly Val Asp Val Pro
545                 550                 555                 560

Asn Ala Ser Leu Met Ile Ile Asp Asn Pro Glu Arg Leu Gly Leu Ala
                565                 570                 575

Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
            580                 585                 590

His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Met
        595                 600                 605

Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
    610                 615                 620

Arg Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
625                 630                 635                 640

Thr Gly Ser Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
                645                 650                 655

Met Ile Pro Glu Val Gln Arg Val Ala Arg His Leu His Gln Gln Tyr
            660                 665                 670

Pro Glu His Ala Lys Ala Leu Ile Glu Arg Trp Leu Pro Glu Arg Val
        675                 680                 685

Arg Tyr Thr Asn Ala
    690


<210> 56
<211> 1220
<212> DNA
<213> Yersinia pestis

<400> 56
atgaacagtg aaaaaaaga acatcttaat acagtatcaa gaaagttaag aacgatcatg 60
gagcgtgata atattgatgc tgtcattgtg acaacgtgtg ataattttta tcatgttacc 120
ggtattctca gtttttttat gtataccttt cgaatacggg cacggctatc gccgttgtct 180
tccgtgatgt gaaaattcca tcgctaatca ttatgaatga atttgaagca gccagcttaa 240
cgttggatat gccaaatgct gaattaaaga cctttcctgt ttgggtagat gtagatgatc 300
cgtttaacat gcgcgattct gcaaataata ataaagagag gccgataggt cctcctattg 360
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agagtgtatg taatatactc aaagacgcat tgaacgatgc cagggtactt aataaaaaaa 420
tagcaataga cctcaatata atgtcaaacg gtggtaaaag agttattgat gccgttatgc 480
ctaatgttga ttttgtcgac tcaagctcta tattcaacga gctaagagtg ataaaaagcc 540
cttgggaaat taaaagactc agaaaaagtg cagaaattac ggaatatggg atcactgaag 600
catcaaagct catccgggta ggatgcacat cagctgaact cactgccgca tataaggcag 660
cagtaatgag taaatctgaa actcactttt caagattcca tcttatctct gttggcgctg 720
atttttcacc caaactcata ccaagcaata ctaaagcctg ttcaggcgac ttaattaaat 780
ttgattgcgg cgtcgatgtt gatggttatg gtgccgatat tgccaggact tttgttgttg 840
gggaacctcc cgagatcacc cggaagatat accaaacaat aagaactggg catgaacata 900
tgctgagtat ggttgcgcct ggcgtcaaaa tgaaagatgt atttgattca acgatggagg 960
tcattaaaaa gtccgggtta cctaattata acagagggca tcttgggcat ggtaatggcg 1020
tctttttggg attagaagag agtcccttcg ttagcactca tgctacagaa tcgttcactt 1080
caggtatggt gctaagttta gaaacacctt actacggcta taatttgggt tcgattatga 1140
ttgaagatat gattttaata aataaagagg gtattgagtt tttgagtaaa ttacccaggg 1200
atttagtttc ttttaattaa 1220

<210> 57
<211> 965
<212> DNA
<213> Yersinia pestis

<400> 57
atggataaga aacgcgtatt tattgccggg catcgtggca tggtgggttc tgctattgta 60
cgtcaacttg aaaaccgtaa tgatattgag ttgatcatta gggatcgtac tgaacttgac 120
ctcatgtctc aatccgctgt gcaaaaattt tttgctactg aaaaaattga tgaaatctat 180
ttggctgcgg caaaagtggg gggattcagg ccaataataa ttatccggca gagttcatct 240
accaaaactt aatgatcgag tgcaatatta ttcacgcggc tcatttagct ggcattcaaa 300
aattattatt tttggggtct tcttgtattt atccaaaatt ggctgcacaa ccaatgacag 360
aggaggctct gttaactggc gtcttggaac caacgaatga accttatgcc atcgccaaga 420
tagccggtat caaactgtgc gaatcttata atcgtcaata tggtcgcgat tatcgcagtg 480
ttatgccaac caacctttat ggtgaaaatg acaattttca ccccgaaaat tcccatgtca 540
ttcctgcctt attacgtcgc ttccatgagg ctaaaattcg taatgataag gaaatggttg 600
tgtggggaac gggtaaacca atgcgtgagt tcctgcatgt agatgatatg gctgctgcca 660
gtgtgcatgt catggagctg tctgatcaaa tttatcaaac caatactcaa ccaatgcttt 720
cgcatattaa tgtcggaacg ggtgtggatt gcactattcg tgaattggca gaaactatgg 780
ctaaagttgt tggtttcacc ggaaatttag tttttgattc aactaagccg gacggaacac 840
cacgaaaatt gatggacgta agccgcttgg ctaaactcgg gtggtgttat cagatttcgc 900
ttgaagtagg tttaacgatg acttatcaat ggttcttggc tcatcagaat aacttcagaa 960
aatag 965

<210> 58
<211> 1076
<212> DNA
<213> Yersinia pestis

<400> 58

atgattaata atagtttctg gcaaggtaaa cgggtttttg taacaggcca tactgggttt 60
aaaggtggct ggttgagttt atggttgcaa accatggggg caacggtaaa aggttactct 120
ttgccccccc ccccacggtg cctagcctat ttgagaccgc acgagttgcc gacgggatgc 180
aatcggaaat cggtgatatt cgtgatcaaa acaaattatt agaatcaatc cgcgaattcc 240
aaccagagat tgttttccac atggctgctc agccactggt ccgtctatcc tattccgagc 300
ctgttgaaac ctactcgacg aatgttatgg gtaccgttta tttactggaa gctattcgcc 360
atgttggtgg cgtcaaagcg gtggtcaata tcaccagtga taaatgctac gataataaag 420
agtggatctg ggctatcgc gaaaatgaag cgatgggggg gtatgatcct tactccaaca 480
gtaaaggttg tgcggaatta gtgacgtcat cctaccgtaa ttcgttcttc aatccagcga 540
actatggcca gcatggcact gccgtagcga cagtgcgtgc gggtaatgtt atcggtggtg 600
gcgattgggc attggatcgc atcgttccag atattcttcg ggcgtttgaa cagtcccaac 660
cagtgattat tcgcaaccca catgccattc gcccatggca gcatgtgttg gagcctttgt 720
cgggttattt gctgttggca cagaagttat atactgacgg tgctgaatat gccgaaggtt 780
ggaactttgg tcctaacgat gctgatgcta ctccagtaaa aaacattgtt gaacaaatgg 840
tgaaatattg ggagagggt gcaagctggc aattagatgg caatgctcac cctcatgaag 900
ctcattatct gaaactggat tgttcaaaag ctaaaatgca acttggctgg catcctcgct 960
ggaacttgaa tactacgctc gaatatattg tgggctggca caagaactgg ttatcaggca 1020
cagatatgca tgaatacagt attactgaaa ttaataatta catgaacact aaatga 1076

<210> 59
<211> 220
<212> DNA
<213> Yersinia pseudotuberculosis

<400> 59
gtgctgaagc aacgcagaga agacaaagaa tacaatacca aaaatcttca ttaaaacgct 60
atatgttatt atctcactag gttttaaaac ttgggacatt actatgtaat cagtctgaat 120
aataattgta gttaaaatag aaaaaattag aaaaccagag gcacgacgga caataggctt 180
aataatatca gatctaattc tacgaagctt gcatgcctgc 220

<210> 60
<211> 265
<212> DNA
<213> Yersinia pseudotuberculosis

<400> 60
ttcgccgagg gatatcactc cgcaaatacc accggcatag agacaatctc gccacgcctt 60
gccgtctttt agcgttacga gagcggccag gcagatcgaa gcgccgacac cgtaaatagt 120
gtgcccgtca caccagcggg ataaataatt tcagcaagat cgctatcaac ataatcccaa 180
cccctgcgcc aaatggctta caggatttgt gggggcaagc gtggtttctg gataaaggcc 240
agcggctagg ccgaattcga gctcg 265

<210> 61
<211> 571
<212> DNA

<213> Yersinia pseudotuberculosis

<400> 61
tcaataaggt gtacgcgcct gagttggaaa ttgaagtaaa aaactaacac aacggttacg 60
ggcaattgac aataattcta ttgaacaatt tcttattctg cgtcgtcatt atctgccgca 120
tgaaaatgac gatatagaaa gtctggcccg tgccgtttgg ttagataacc gttattggga 180
taatacccgt atttctattg ccaatggaat tggtctggca tttaaaggcg attaatgaaa 240
agtctcgatt ttaccttaag catgattgat aaaatcacac ggccattaaa atccgtgcaa 300
gcctctgtaa aaggatttgc ggaaagttct caggcggctt tcggtaaaat tgccattggc 360
ggggccgcgc tgttcggtgt cgtacaggga atgaagggcg cactgggacc cgcagctgaa 420
tttgccggcg cgcttaatga ggccagcgcc aagggcgtga gtgattgcgc cttgcaaaag 480
atgagcgctg acgccctgaa attcagtatg caatatggcc gcagcgccgt gggatgttgt 540
gcgttcaaat gcagacatgg cgcaagtgca a 571

<210> 62
<211> 423
<212> DNA
<213> Yersinia pseudotuberculosis

<400> 62
aagccacagt tatcttgatg tggacattat gcattgtaat agcccattaa catgcgctaa 60
gaagcataaa ttaatataca gtaacaagca ttacgaggtg ctaatgtttg gaaagcagcc 120
tcttccaact acaataataa gttaactatc ctccacccac aaataattac aaatgacccc 180
tttccgctat aactccgatc tcaccagcgg ctcgctacaa acccgagagt gtcgcattat 240
tactggcttg ttactccaag agcttgatga agctgcctgg gataaagcca tgtataagga 300
aaatgtgctt cagaaacgca cgcaatctac ggtaagacgt atttcttcag cgcttagaaa 360
acgcctagaa cacctaagct ctgacttttg ggcttttgcg tttttatgct aggccgaatt 420
cga 423

<210> 63
<211> 380
<212> DNA
<213> Yersinia pseudotuberculosis

<400> 63
gctgagtagc ctgatatttt tatggtgaaa aagataaaca atcatagagg ggataaatat 60
gagccagttc taccattgtt cagataagtt taagcaagat actgtcaatc acagtgacca 120
ttcatggtca ttacacttcc tccagttgcc agacaatgcc taacataaaa acgcaaaagc 180
ccaaaagtca gagcttaggt gttctaggcc taatccaagc tcggaagaaa tacgtcttac 240
cgtaaattgc gtgcgtttct gaagcacatt ttccttatac atggctttat cccaggcagc 300
ttcatcaagc tcttggagta acaagccagt aataatgcga cactctcggg tttgtagcga 360
gccgctggtg agatcggagt 380

<210> 64
<211> 243

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<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(243)

<400> 64
atg gaa aca aga ttc cta cag gca aac aaa gaa gca cgc tgg gcc ttc      48
Met Glu Thr Arg Phe Leu Gln Ala Asn Lys Glu Ala Arg Trp Ala Phe
1               5                   10                  15

ggc tta aca ctg gcc tac ctc gca ggg tgg att ata acc gct tac tta      96
Gly Leu Thr Leu Ala Tyr Leu Ala Gly Trp Ile Ile Thr Ala Tyr Leu
            20                  25                  30

ccg ggc aac ctt ccc gga atg agc ggc cta cct gct tgg ttt gaa gcg      144
Pro Gly Asn Leu Pro Gly Met Ser Gly Leu Pro Ala Trp Phe Glu Ala
        35                  40                  45

gcc tgt atc gca tta ccg ctc ctg ttt att gtg ctg tgt att ctg atg      192
Ala Cys Ile Ala Leu Pro Leu Leu Phe Ile Val Leu Cys Ile Leu Met
    50                  55                  60

gtg cgg ctg ata ttc cgc gat att cca ctg gag gat gac gat gca aac      240
Val Arg Leu Ile Phe Arg Asp Ile Pro Leu Glu Asp Asp Asp Ala Asn
65                  70                  75                  80

tga                                                                   243


<210> 65
<211> 80
<212> PRT
<213> Yersinia pestis

<400> 65
Met Glu Thr Arg Phe Leu Gln Ala Asn Lys Glu Ala Arg Trp Ala Phe
1               5                   10                  15

Gly Leu Thr Leu Ala Tyr Leu Ala Gly Trp Ile Ile Thr Ala Tyr Leu
            20                  25                  30

Pro Gly Asn Leu Pro Gly Met Ser Gly Leu Pro Ala Trp Phe Glu Ala
        35                  40                  45

Ala Cys Ile Ala Leu Pro Leu Leu Phe Ile Val Leu Cys Ile Leu Met
```

```
        50                                  55                                  60

Val Arg Leu Ile Phe Arg Asp Ile Pro Leu Glu Asp Asp Asp Ala Asn
65                  70                  75                  80
```